STIC-Biotech/ChemLib

From: Sent: To: Subject:

Whiteman, Brian Monday, April 28, 2003 10:43 AM STIC-Biotech/ChemLib seq search

09/818,943 3/28/01 Eriksson et al.

search seq id nos: 1 and 2 against us patent and us patent application databases.

Claiming a transgenic mouse comprising a nucleotide encoding either seq id no: 1 or 2.

Thanks,
Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
Crystal Mall 1, 11A16
(703) 305-0775

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-302-2034

Searcher:
Phone:
Location:
Date Picked Up: 4/29,
Date Completed: 4/29
Searcher Prep/Review: /
Clerical:
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TYPE OF SEARCH:	
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Structures:	_
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/ENDOR/COST (where applied	c.)
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Sequence 2, Appli	-	-	•	•	Sequence 5, Appli	•	Sequence 5, Appli	•	•	Sequence 3, Appli	•	•	`	`	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli

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; ORGANISM: Human US-09-040-220D-2
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US-09-040-220D-2
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APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.

TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID SEQ ID NO 2
LENGTH: 345
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Best Local Similarity
Matches 343; Conserv
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FILE REFERENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT FILING DATE: 1998-03-17
CURRENT FILING DATE: 8
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                      LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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CURRENT APPLICATION NUMBER: US/09/265,686; CURRENT FILING DATE: 1999-03-10; PRIOR APPLICATION NUMBER: US 09/040,220; PRIOR FILING DATE: 1998-03-17; PRIOR APPLICATION NUMBER: US 09/184,216; PRIOR FILING DATE: 1998-11-02; NUMBER OF SEQ ID NOS: 8; SEQ ID NO 2; SEQ ID NO 2; NUMBER: 345
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Best Local Similarity
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APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
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APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS
FILE REFERENCE: P1122P2
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CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
ORGANISM: Human
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Pred. No. 4.8e-193;
2; Mismatches 0;
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SOFTWARE: FastSEQ for
SEQ ID NO 5
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Best Local Similarity
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Best Local Similarity 99.4%;
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APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER APPLICATION NUMBER: US 60/180,169
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 4.8e-193;
2; Mismatches 0;
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Pred. No. 4.8e-193;
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Sequence 37, Application US/09457066
Patent No. 6433673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
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US-09-457-066-43
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Best Local
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APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
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CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Hart, Charles
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86.7%;
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Pred. No. 1.1e-172;
28; Mismatches 18;
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; Sequence 2, Application US/09540224
; Patent No. 6468543
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                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
APPLICANT: HATC, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
FULLE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
                                  Query Match
Best Local Similarity
Matches 159; Conserv
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SEQ ID NO 2
LENGTH: 370
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Best Local Similarity
Matches 159; Conserv
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 37
LENGTH: 370
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CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
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TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
                                                                                                                                                   TYPE: PRT
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3 LFGLLLVTSALAGQRRGTQAESNLSSKFQFSSN---KEQNGVQD-PQHERIITVSTNGSI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGVRGLHKSLTDVALEHHEE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL-LEDFQPAAASETN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYL
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                                      59;
                                  Score 741.5; DB 4;
Pred. No. 3.1e-72;
9; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 741.5; DB 4; Pred. No. 3.1e-72;
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                                                                     Length 370;
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LENGTH: 370
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE, TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4 FILE REFERENCE: 00-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gilbertson, Debra G. APPLICANT: Hart, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
 258
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                                                                                                                                                                                                                WRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEC
                                                                                                                                                           QISKGNQIRIREVSDEYFPSEPGFCIHYNIVMPQFTEAV-----
                                                                                                                                                                                                                                                                                       QRASIKALRNANLR-----RDESNHLTDLYQREENIQVTSNGHYQSPRFPNSYPRNLLLT 80
                                                                                                                                                                                                                                                                                                          QRRGTQAESNLSSKFQFSSNKEQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLV 74
                                                                   ITDPT-LTADALDKTVAEFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK 257
                                                                                          VLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSR 234
                                                                                                                                            ITSRTNQIKITEKSDDYFVAKPGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL-LEDFQPAAAASETN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV----- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT 118
 - VDLDRLNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHER 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKGNGYV
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                                                                                                                                                                                                                                                                                                                                                             39.7%; Score 737.5; DB 4;
44.0%; Pred. No. 8.4e-72;
ative 59; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  370;
                                                                                                                                                                              -----SPS 174
                                                                                                                                                                                                                                                                                                                                                             Gaps
316
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US-08-872-757-2
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                                                                                                                                                                                                                                                                ; MOLECULE TYPE: US-08-872-757-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08872757
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patebilin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/ACENT INFORMATION:
NUMBER: ALBURY ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-854-3660
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705
                                                               654
                                                                                                114
                                                                                                                                  599
                             172 SPSVLPPSALPLDL 185
                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Halluin, Albert P. REGISTRATION NUMBER: 25,227 REFERENCE/DOCKET NUMBER: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 10036-2711
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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Penuse of the
                                                                                                                                                            55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                               GLTAHSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF----FSEN-
                                                                                            --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV 171
                                                                                                                               NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG-----NDVCKYDFVEVRS
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RPALQPPRGPPHQL
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                                                                                                                                                                                                                                                                                                                                 730 amino acids
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36.68;
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                                                                                                                                                                                                           Score 172.5; DB 4
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                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                              DB 4;
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RESULT 10 US-08-572-225-1 ; Sequence 1, Application US/08572225

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Matches
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                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                   Sequence 18,
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                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/572,225
FILING DATE: 13-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
                                                                                            TITLE OF INVENTION: Semaphorin Receptors NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                               APPLICANT: He, Zhigan
APPLICANT: Chen, Hang
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                  456 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 502
                                                                                                                                                                                                                                                                                                                                                    114 -- PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                   401 NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG-----NDVCKYDFVEVRS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                 55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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               COUNTRY:
                                 STATE:
                                               CITY: HILLSBOROUGH
                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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94010
                               CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66141 PENNIE
                                                                                                                                                                                                                                   Application US/08936135
                                                                E: SCIENCE & TECHNOLOGY LAW GROUP 75 DENISE DRIVE
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Li, Shi-Wu
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RESULT 12
US-08-936-135-20
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Patent No. 6054293
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: #loppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 909 amino acid
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: He, Zhigang APPLICANT: Chen, Hang
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH
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                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                  COUNTRY: UZIP: 94010
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TOPOLOGY: lir
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                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                   STATE:
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(650) 34
                                                                                                                                                                                                                                                               USA
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SYSTEM: PC-DOS/MS-DOS
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linear
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                  UC97-288-2
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Pred. No. 7.
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Patent No. 6428965
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Best Local Similarity
   Query Match
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                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acid
                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
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APPLICANT: Ginty, David
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                                                            STRANDEDNESS:
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                                                                                                                                                                                                                NAME: Kagan, Sarah A
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
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                                                                                          922 amino acids
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1001 G Street, NW
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OR SEQ ID NO: 20:
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                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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   8.8%;
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   Score 163.5;
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Length 922;
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US-09-374-135-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09116473 Patent No. 6428965 GENERAL INFORMATION:
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Best Local Similarity
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Matches 42; Conservative
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CURRENT FILING DATE: 1999-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TYPE: PRT
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                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kolodkin, Alex APPLICANT: Ginty, David
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                    COMPUTER: IBM CONTROL OPERATING SYSTEM: SOFTWARE: FastSE(
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Leong, Kahan
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Saffran, Douglas C.
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6: Mismatches 50;
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SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.8%; Score 163; DB 4; Length 925; Best Local Similarity 33.8%; Pred. No. 1.1e-08; Matches 45; Conservative 20; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/116,473
FILING DATE: 17-JUL-1998
CLASSIFICATION:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/052,762
FILING DATE: 17-JUL-1998
ATTORNEY/ACENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.74973
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                129 ARQGAGESLRYEI 141
                                                                                                                                              150 FPSEPGFCIHYNI 162
                                                                                                                                                                                            92 EREGLEDPEDDICKYDFVEVE--EPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEY 149
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| 74 PHFEIEKHD---CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSP-Y 128
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Result
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Maximum DB
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 seq length: 0 seq length: 2000000000
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Listing first 45 summaries
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   /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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KW Grb 30-SEP-1998; 12-NOV-1998; 03-DEC-1998; 18-DEC-1998; 21-MAY-1999; 15-JUL-1999; Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; Lung 30-SEP-1999; 06-APR-2000 WO200018212-A2 Homo sapiens. 25-JUL-2000 AAY84557; AAY84557 standard; Protein; 345 (LUDW-) LUDWIG INST CANCER RES. Amino acid sequence of platelet-derived growth factor C (PDGF-C). carcinoma; erythroleukemia; tissue (first entry) 98US-0102461. 98US-0108109. 98US-0110749. 98US-0113002. 99US-0135426. 99US-0144022. 99WO-US22668 A remodelling

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PDGF-C polypeptides can be used in pharmaceuticals for promoting cell provides and polypeptides can be used in with one other growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                          the cell into a non-human animal and allowing the cell into a non-human animal. The transgenic animal is useful as a a transgenic, non-human animal. The transgenic animal is useful as a model to study disease states characterised by over-expression of pDGF-C and to find therapy for those diseases, particularly hypertrophy and and to find therapy organs including the heart. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses a method for producing a transgenic, non-human animal over-expressing a platelet derived growth factor C (PDGF-C), or its functional fragment or analogue. The method involves introducing a transgenic PDGF-C DNA into a cell of a non-human animal, introducing a transgenic PDGF-C DNA into a cell of a non-human animal, introducing into a non-human animal and allowing the cell to develop into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A transgenic animal over-expressing platelet derived growth factor useful to study and find therapy for disease associated with PDGF-cover-expression, including cardiac hypertrophy and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                     GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                            VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                                                                             LPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                       GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                                                                                                                                                                                                                             PREPHTYPRNTVLVWRLVAVEENVWIQLTEDEREGLEDPEDDICKYDEVEVEEPSDGTIL
                                                                                                                                                                                                                                            PREPHTYPRNTVLVWRLVAVEENVWIQLTEDEREGLEDPEDDICKYDFVEVEEPSDGTIL 120
LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                                                                                              LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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ilarity 100.0%;
Conservative
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Pred. No. 1.7e-179;
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RESULT 3
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CC therapeutically, especially by expressing encoding polynucleotides, to contract cardiovascular or endothelial disorders in mammals, especially contracts and may especially be used to treat cardiac hypertrophy contracts and may especially be used to treat cardiac hypertrophy contracts and be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to contract disorders and agonists, and the antagonists administered to contract antagonists and agonists, and the antagonists antagonists are also caseful therapeutically as antagonists, as above. The antibodies are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. cancer or consequent disease, or neovascularization associated with tumor formation). By contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding contacting the antibody with a tissue sample and detecting formation contains antibody-VEGF-E polypeptide complex. Polynucleotides encoding contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding contacting abnormally high or low VEGF-E gene expression in contact and contact and conditions and contact and conditions and conditions are also be used to amutated form of VEGF-E (e.g. a) cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting among an used to produce probes useful to detect related complex. Polymer may also be used to amutated form a cardiovascular and endothelial or angiogenic disorder such as a tumor), by detecting among and the veget to dispense a disease or cardiovascular and endothelial or angiogenic disorder such as a tumor), by detecting and the veget to produce probes useful to detect related contracting the veget to produce
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Matches 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New growth factor polypeptide useful for treating cardiovascular endothelial disorders, e.g. cardiac hypertrophy -
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                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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02-NOV-1998;
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MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                    MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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98US-0079728.
98US-0079786.
98US-0079920.
98US-0079923.
98US-0080105.
98US-0080165.
98US-0080194.
98US-0080328.
98US-0080333.
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98US-0079689.
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31-SEP-1998;
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22-APR-1998;
22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1998;
23-APR-1998;
23-APR-1998;
27-APR-1998;
                                 New secreted and transmembrane polypeptides and their polynucleotides useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
                                                                                                             (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-APR-1998;
9-APR-1998;
9-APR-1998;
                                                                    1999-551358/46.
DB; AAZ34296.
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                                                                                                               GENENTECH INC
                                                                                             Goddard A,
                                                                                                                              9805-0083545.
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9805-0084414.
9805-0084458.
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98US-0082796.
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98US-0081195
98US-0081203
98US-0081229
98US-0081817
98US-0081831
98US-0081952
98US-0081955
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98US-0083322
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                                                                                             ΚP,
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The Claim 12;

present

Fig

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530pp; English

describes secreted and

transmembrane polypeptides

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RESULT 5
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Best Local Sim
Matches 343;
                                                      31-AUG-1998;
27-JAN-1998;
05-JUN-1998;
24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generatic of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                            tissue growth inhibition; tumour growth angiogenesis; coronary artery blockage
                                                                                                                                                                                                                       Vascular endothelial growth factor related protein; VEGF-R protein; tissue growth inhibition; tumour growth; cancer; tissue growth;
         Dou S,
                                                                                                                  26-JAN-1999;
                                                                                                                                                                                                                                                        Human vascular endothelial growth factor related protein.
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                                                                                                                                                                                                                                                                                                                                 AAY30023 standard; Protein;
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98US-0072635.
98US-0088089.
98US-0090544.
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         YHY;
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Pred. No. 8.9e
2; Mismatches
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.9e-179;
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RRESULT 6
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Matches 343;
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                                                                                                                                                                                                                        Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB48657 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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related (VEGF~R) prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                               sapiens
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Pred. No. 8.9e
2; Mismatches
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3.9e-179;
hes 0;
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240 240

LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK

LTEEVRLYSCTPRNESVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK

181

241

121

121 61 61

GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA

180

120

GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA

Query Match Best Local : Matches

Similarity

99.68;

Score 1851; Pred. No. 8

DB 21; 3.9e-179;

345; 0;

Conservative

2;

Mismatches

Indels Length

Gaps

0

1 MSLFGLLLYTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS

MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS

60 60

PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120

PREPHTYPRNTVLVWRLVAVEENVWIQLTEDERFGLEDPEDDICKYDFVEVEEPSDGTIL

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The invention relates to the human growth factor homologue zvegf4 (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member CC of the PDGF (platelet-derived growth factor) VEGF (vascular endothelial CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654) CC characterised by a PDGF cystine knot structure. Zvegf4 has CUB domain CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like CC growth. The invention also relates to fusion proteins comprising human CC zvegf4 or fragments thereof, particularly human zvegf4 has proteins comprising human CC zvegf4 or fragments thereof, particularly human zvegf4; an antibody CC which binds to human zvegf4 or a fragment thereof; a method of acilivating cells comprising human ccells comprising human cvegf4 or a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface PDGF receptor using a zvegf4 derived polypeptide; a cell-surface polypeptides; and a method of detecting a genetic cells comprising exposing bone cells comprising because of a patient. Zvegf4 proteins and derived cells comprising polyperation or cells comprising polyperation or cells compair or the treatment or repair or the treatment of liver damage, and may also be used to stimulate treatment of Alzheimer's disease or matter compair or the treatment of periodontal disease and fractures. They may be used in the treatment of periodontal disease and fractures. They may also be used to the polyperation or proliferation of periodontal disease and fractures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor homologs and the nucleic acids that encode them, e.g. for treating liver damage, ischemia, multiple sclerosis a
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10-NOV-1999; 99US-0164463
04-FEB-2000; 2000US-0180169
                                            used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. for treating 1: Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilbert T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2000;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-687541/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 125-126; 143pp; English
345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US40047
AA;
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RESULT 7
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Best Local :
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LP8 or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LP8 antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LP8 are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                     Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist
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                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for enhancing tissue
                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 63-64; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200059940-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis;
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                      MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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LPLDLLNNATTAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                                                            called
                                                                      PREPHTYPRNTVLVWRLVAVEENVWIQLTEDEREGLEDPEDDICKYDEVEVEEPSDGTIL
                                                                                    PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-664991/64.
                                                                                                                       MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            latelet derived growth factor related protein; LP8; VEGFh; endothelial growth factor h; tissue regeneration; vulnerary; lerosis; PDGF-related protein; antiarteriosclerotic.
                                                                                                                                                                                                                                                         lerosis.
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                                                                                                                                                                                                                                              VEGFh.
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                        The present sequence
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                                                                                                                                                                      Pred. No. 8.9
2; Mismatches
                                                                                                                                                                                Score 1851; DB 21;
Pred. No. 8.9e-179;
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                                                                                                                                                                                          Length
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RESULT 8
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16-DEC-1999;
30-DEC-1999;
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21-APR-1999;
28-APR-1999;
14-MAY-1999;
23-JUN-1999;
                                                                                                                                        Ferrara
Goddard
Kljavin
AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane polypeptides. The PRO polynucleotides and polypeptides have cytoactivity. The polynucleotides and polypeptides can be used for discretivity.
                                               Claim
                                                               Novel PRO polypeptides and polto target bioactive molecules cellular activities -
                                                                                                     N-PSDB;
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05-JAN-2000;
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                                                                                                                                                                                                                                                                                         26-JUL-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                         08-MAR-1999;
12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB44322 standard; Protein;
                                                                                                                                 Shelton
                                                                                                                                                                    Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2000;
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                                                                                                    2000-611443/58.
DB; AAC78582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                               12;
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IJ,
                                                                                                                                                                                      GENENTECH INC.
                                              Fig
                                                                                                                               AJ, Baker KP,
Filvaroff E,
Godowski PJ,
Kuo SS, Nap,
Stewart TA,
                                                                                                                                                                                                        99WO-US31274.
2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNQ174) protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US04341
                                                                                                                                                                                                                                            99US-0145698.
99US-0162506.
99WO-US28313.
99WO-US28551.
99WO-US28565.
99WO-US30095.
                                                                                                                                                                                                                                                                                                            99US-
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99US-0130232.
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                                                                                                                                                                                                                                                                                                                                                         99WO-US05028
99US-0123957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                             636pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tag; detection;
                                                                                                                                                                                                                                                                                                             -0141037
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                                                                                                                                         Napier MA,
                                                                                                                               Botstein D, Desnoye
Fong S, Gao W, Gez
Grimaldi CJ, Gurney
Pier MA, Pan J, Paor
Tumas D, Williams F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane protein; PRO;
                                              English
                                                                         polynucleotides used in detection methods, les to specific cells, and to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345
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W, Gerber H,
                                                                                                                                         Gurney AL,
, Paoni NF,
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                                                                                                                                 PM,
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                                                                                                                               F, ROY MA;
Wood WI;
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                                                                                                                                                           Eaton DL;
Gerritsen
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for detecting cytostatic

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Best Local
                                                                              22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                            Gordon RD,
                                                                                                                                                                                     WO200037641-A2
                                                                                                                                                                                                                                    angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                       VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
                                                                                                                                                                                                                                                                                                                                Human RACE generated VEGF-X protein
                                                                                                                                                                                                                                                                                                                                                                                                               AAB10633 standard;
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                                                                                                                                                                                                               Homo
                                                                                                                                  21-DEC-1999;
                                                     (JANC ) JANSSEN PHARM NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRWCGSGTVPGKQISKGNQIRIREYSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
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               ,NS
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                           Sprengel JJ,
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                             98GB-0028377.
99US-0124967.
99US-0164131.
                                                                                                                                 99WO-US30503
                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                           Yon
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Pred. No. 8.9e-179;
2; Mismatches 0;
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                          Dijkmans
                           Gosiewska
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DR N-PSDB; AAA71951.

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New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity preventing diseases associated with inappropriate angiogenesis activity preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds.

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Disclosure; Fig 6; 127pp; English.

XX

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and can antidabetic activity and acts as an angiogenesis and vascularization cregulator. An antisense molecule of the invention is useful for treating cregulator. An antisense molecule of the invention is useful for treating cregulator. An antisense molecule of the invention is useful for treating cregulator. An antisense molecule of the invention is useful for treating cregulator. An antisense molecule of the invention of new blood crescels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful cressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair by promoting angiogenic activity or vascularization. This sequence repairs by promoting angiogenic activity or cresularization. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
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Matches
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Best Local
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VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
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343; Conserv
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Pred. No. 8
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1.9e-179;
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RESULT 10
AAB10635
ID AAB106
XX AB10
AC AAB10
XC AAB10
XC AB10

AAB10635; 19-JAN-2001

(first entry)

Human VEGF-X protein #1 isolated from clones 4 and

AAB10635 standard;

Protein;

345

AA

antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

skin graft growth

vascular endothelial growth factor; human; vulnerary;

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Best Local Similarity
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18-MAR-1999;
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                                                                         LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
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DB; AAA71955.
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                                                       GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
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, Xu J;
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99US-0124967.
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Pred. No. 8
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3.9e-179;
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61 <u>,,,</u>

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PREPHTYPRNTVLVWRLVAVEENVWIQLTEDEREGLEDPEDDICKYDEVEEPSDGTIL

Local Similarity

Conservative

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Indels

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RESULT 11
AAB10644
Query Match
Best Local S
Matches 343
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                   This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an anglogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure scress, venus sores, diabetic ulcers and burns and to promote
                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 30B; 127pp; English.
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antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
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                                                                                                                                                                                                              ascularization.
                                                                                                                                                                          graft growth, tissue repair, proliferation of new blood vessels, ue regeneration and organ repair by promoting angiogenic activity ularization. This sequence represents a human VEGF-X protein ribed in the method of the invention.
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burns; skin graft growth
  Score 1851; DB 21;
Pred. No. 8.9e-179;
2; Mismatches 0;
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X), protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeare the development of tissues, tissue regearenting medicaments for treating wounds such as dermal ulcers,
                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                    RD,
                                                                                                                                                                                                                                                                                                     SN,
                                                                                                                                                                                                                                                                                                   Sprengel, Xu J;
                                                                                                                                                                               Fig 11; 127pp;
                                                                                                                                                                                                                                                                                                                                                                           98GB-0028377.
99US-0124967.
99US-0164131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US30503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial growth factor; human; vulnerary; cytostatic;
ntiarthritic; antipsoriatic; antidiabetic; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                   JJ,
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                                                                                            22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antipsoriatic; antidiabetic; freafment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity of vascularization. This sequence represents the human 990126vegx protein used to illustrate the method of the invention.
            WPI; 2000-442669/38
                                    Dhanaraj SN,
                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                            21-DEC-1999;
                                                                                                                                                                                         WO200037641-A2
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                  19-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                               AAB10651 standard;
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                                                                      (JANC
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                                                                     ) JANSSEN PHARM NV
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99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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No. 8.
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8.9e-179;
                                              JJH,
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CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and CC antidiabetic activity and acts as an angiogenesis and vascularization CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic CC retinopathy by inhibiting angiogenic activity or inappropriate CC vascularization including formation and proliferation of new blood CC vessels, growth and development of tissues, tissue regeneration and organ CC and tissue repair in a subject. The products of the invention are useful CC pressure sores, venous sores, diabetic ulcers and burns and to promote CC skin graff growth, tissue repair by promoting angiogenic activity or consultation. This sequence represents the human VEGF-X protein XX
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Best Local
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                                                                             ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; macular hole; myppia; traumatic chorioretinopathy;
                                                   retinal vision
                                                                                                                                                                  Human PRO200 (vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                PRO200; vascular epithelial growth factor E; VEGF-E; human;
                                                                                                                                                                                                     22-JAN-2001
                                                                                                                                                                                                                                                                    AAB19578 standard; Protein; 345 AA
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                                                                                                                                                                                                   (first entry)
                                                 necrosis syndrome; contusion; edema; n occlusion; vascular disease; retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%;
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Pred. No. 8.9e-179;
2; Mismatches 0;
                                                                                                                                                                  growth factor
                                                   retinal vasculitis
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282..288
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                                                                                                                                               /note= "N-myristoylation" 117...123
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15..21
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254..258
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55..59
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25..29
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15..345
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10-MAR-2000; 2000WO-US06319

12-MAR-1999;

(GETH) GENENTECH INC

Klein z Kljavin Goddard A, Kljavin IJ, Gurney Kuo SS, AL, Hebert C, , La Fleur M, Wood WI; Henzel WJ, Kabakoff RC;

N-PSDB;

Novel PRO polypeptides useful for preventing or rescuing retinal ce from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, uveitis

Claim 2; Fig 2; 140pp; English

producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay. The invention relates to the use of PRO polypeptides to delay. The invention relates to the use of PRO polypeptides to delay. The invention relates to the use of PRO polypeptides to delay. The invention relates to the use retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, amacrine cells, displaced amacrine cells, horizontal and bipolar neurons, and supportive cells (including Mueller cells and pigment epithelial cells) from injury and degradation. The retinal cells are preferably photoreceptors and photoreceptor cell injury or death is caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinitis pigmentosa, macular degeneration, including age-related, retinal detachment, retinal characteristic myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or contusion such as Purtscher's retinopathy, cellagen vascular diseases, thrombocytopenic purpura, uveitis, retinal vascular alseases, thrombocytopenic purpura, clone (see AĀA88515) that was isolated from a glioma cell line G61 library using probes (see AAA88523-26) based on an expressed sequence tag (see AAA88522) that showed homology to VEGF. PRO200 has a predicted mol. wt. of 39,029 and a pl of about 6.06. A method for The present sequence is that of human PRO200 or vascular endothelial growth factor ${\tt E}$ (VEGF-E), as predicted from systemic lupus erythematosus Ø CDNA

Sox

Sequence

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RESULT 15
AAB33414
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10-WAR-1999;
12-WAR-1999;
23-WAR-1999;
12-APR-1999;
20-APR-1999;
28-APR-1999;
04-WAY-1999;
                                                                                                                                                                                                                                                                                                                                                                              Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyrold; antidiabetic; noctropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; systemic vasculitis; autoimmune mediated renal disease; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; inflammatory bowel disease; julten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; reafficences carefet reference to the contraction associated disease; arafficences carefet references to the contraction associated diseas
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343; Conser
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                   99US-0123618.
99US-0123957.
99US-0125775.
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99US-0131445.
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Pred. No. 8.9e-179;
2; Mismatches 0;
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05-OCT-1999
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01-DEC-1999
02-DEC-1999
03-DEC-1999
04-DEC-1999
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06-JAN-2000
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23-JUN 1999
20-JUL 1999
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15-SEP 1999
15-SEP 1999
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99WO-US30995.
99WO-US31274.
2000WO-US00277.
2000WO-US00277.
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2000WO-US03565.
2000WO-US04341.
2000WO-US044414.
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99WO-US12252.
99US-0141037.
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Ashkenazi AJ, Baken Kabakoff RC, Lu Y, Stewart TA, Tumas I , Baker KP, Godurt Lu Y, Pan J, Pennica D mumas D, Watanabe CK, V Gurney AL, ... b, Shelton DL, S Hebert C, Henzel

2000-572271/53. DB; AAC58579.

N-PSDB;

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumato arthritis, osteoarthritis, thyroiditis and diabetes mellitus rheumatoid -

Claim 33; Fig 2; 309pp; English.

The present invention describes sixty four human PRO proteins which can CC be used in the treatment of immune related diseases. The human PRO CC proteins, anti-PRO antibodies, agonists and antagonists are useful for CC treating and diagnosing immune related disorders. The disorders are Steelected from systemic lupus erythematosus, rheumatoid arthritis, costeoarthritis, juvenile chronic arthritis, spondyloarthropathies, Systemic sclerosis, idiopathic inflammatory myopathies, Sjoyren's CC syntemic sclerosis, idiopathic inflammatory myopathies, Sjoyren's CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic canaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, CC immune-mediated renal disease, demyelinating diseases of the central CC and peripheral nervous systems, hepatobiliary diseases, inflammatory CC bowel disease, gluten-sensitive enteropathy and whipple's disease, CC immunological diseases of the lung, and transplantation associated CC diseases including graft rejection and graft-versus-host-disease. CC diseases including graft rejection and graft-versus-host-disease. CC AAC58397 to AAC5878 represent PCR primers and hybridisation probes used C1 in the isolation of human PRO sequences. AAC58679 and protein CC sequences given in the exemplification of the present invention.

345 AA;

Query Match
Best Local Similarity
Matches 343; Conser Conservative 99.6%; 99.4%; Score 1851; Pred. No. 8 Mismatches .9e-179; les 0; DB 21; Length 345; Indels 0; Gaps

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Search completed: April 29, 2003, 09:05:43 Job time: 34.5 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1858
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and is derived by analysis of the total score distribution score greater than is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	, U	4	w	N	1	Result
1851	1851	1851	1851	1851	1851	1851	1851	1851	1851	1851	1851	1851	1851	1851	1858	1858	1858	1858	Score
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US-10-103-197-4	US-10-176-921-286	US-10-176-918-286	US-10-175-746-286	US-09-796-753-6	US-10-140-470-286	US-10-123-904-286	US-10-121-049-286	US-10-028-072-286	US-09-978-189-488	US-09-999-832A-488	US-10-139-583-2	US-09-978-192A-488	US-09-978-697-488	US-09-978-295A-488	US-09-818-943-1	US-10-260-539-32	US-10-086-623-32	US-09-852-209A-3	ID
	Sequence 286, App	`	Sequence 286, App	Sequence 6, Appli	Sequence 286, App	Sequence 286, App	Sequence 286, App	Sequence 286, App	Sequence 488, App	Sequence 488, App	Sequence 2, Appli	Sequence 488, App	Sequence 488, App	Sequence 488, App	Sequence 1, Appli	Sequence 32, Appl	Sequence 32, Appl	Sequence 3, Appli	Description

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286,	,986	88,	88	, 88	88,	88,	, 38	.86	88,	88,	88,	, 38	, 88	88,	88,	88,	88	88,	386,	88	, 98	, 98	, 98	, 98	, 98
App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	Αpp	App	App	App	App

ALIGNMENTS

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APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, MARKO
APPLICANT: ALITALO, KARI
APPLICANT: ALITALO, KARI
APPLICANT: OESTMAN, ARNE
APPLICANT: HELDIN, CARI-Henrik
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR APPLICATION NUMBER: 09/410,349
                                                                                           ; ORGANISM: Homo sapiens US-09-852-209A-3
                                                                                                                                   SEQ ID NO 3
LENGTH: 345
TYPE: PRT
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Best Local Similarity
Matches 345; Conserv
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                                                                                                                                                                                                   SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-07-15
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/144,022
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/135,426 PRIOR FILING DATE: 1999-05-21
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5. US20020164687A1
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                         100.0%;
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Score 1858; DB 9;
Pred. No. 2.6e-161;
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APPLICANT: LI, XUII

APPLICANT: UUTELA, MARKO

APPLICANT: ALITALO, KARI

APPLICANT: ALITALO, KARI

APPLICANT: ALITALO, KARI

APPLICANT: ALITALO, KARI

APPLICANT: PELDIN, CARI-Henrik

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA

FILE REFERENCE: 1064/44833C2

CURRENT APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 60/113,997

PRIOR APPLICATION NUMBER: US 60/113,997

PRIOR RILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: US 60/150,604

PRIOR RPILICATION NUMBER: US 60/157,756

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 2000-10-19
                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid sequence
US-10-086-623-32
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US-10-086-623-32
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 42
SOFTMARE: PATENTIN VERSION 3
SEQ ID NO 32
LENGTH: 345
TYPE: PAT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                      Query Match
Best Local :
                                                                                    Matches
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APPLICANT: AASE, Karin
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                                                                                    Conservative
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                                                                                  Score 1858; DB 9;
Pred. No. 2.6e-161;
; Mismatches 0;
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APPLICANT: PONTEN, Annica
APPLICANT: PONTEN, Marko

APPLICANT: UUTELA, Marko

APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: HELDIN, Cari-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DN/
FILE REFERENCE: 1064/44833C2

CURRENT APPLICATION NUMBER: US/10/260,539

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US/10/086,623

PRIOR FILING DATE: 2000-03-04

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-11-0

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1998-12-28
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                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR APPLICATION NUMBER: US 99/438,046
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR APPLICATION NUMBER: US 09/691,200
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APPLICANT:
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Best Local Similarity
Matches 345; Conserv
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SOFTWARE: PatentIn version
SEQ ID NO 32
LENGTH: 345
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                                                                                  Score 1858;
Pred. No. 2.6
0; Mismatches
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2.6e-161;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-818-943-1
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US-09-818-943-1
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APPLICANT: LI, HONG
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: (PDGF-C) AND USES THEREOF
FILE REFERENCE: 1064/48487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
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Best Local Similarity
Matches 345; Conserva
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Patent No. US20020049987A1
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PRIOR SEQ ID NOS: 7
SOFTWARE: DATA: 2000-03-28
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CURRENT FILING DATE: 2001-03-28
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APPLICANT: LI, XUII
APPLICANT: PONTEN, Anni
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PONTEN, Annica
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Conservative 0
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Pred. No. 2.6e-161;
; Mismatches 0;
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US-09-978-295A-488
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/91858
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065364
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Shelton, David L.
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Desnoyers, Luc
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C27
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                                                                                                  APPLICATION NUMBER: 60/
FILING DATE: 1998-03-11
        APPLICATION
                          FILING DATE:
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Shelton, David L.
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Paoni, Nicholas F.
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kljavin, Ivar J.
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Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
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PRIOR APPLICATION NUMBER: 60/081203
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PRIOR APPLICATION NUMBER: 60/081229
PRIOR TILING DATE: 1998-04-09
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PRIOR APPLICATION NUMBER: 60/079728
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PRIOR APPLICATION NUMBER: 60/081071
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PRIOR APPLICATION NUMBER: 60/079920
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PRIOR APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/084600
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                                                                                   60/085573
APPLICANT: Shetton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 00/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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US20020177553A1
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Baker Kevin P.
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Gao, Wei-Qiang
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f, Ellen
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DR FILING DATE: 1998-04-15
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OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080328

OR FILING DATE: 1998-04-01

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OR APPLICATION NUMBER: 60/080334

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OR APPLICATION NUMBER: 60/080334

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080334

OR FILING DATE: 1998-04-01

ARPLICATION NUMBER: 60/079923
OR ETLING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/080105
OR APPLICATION NUMBER: 60/080105
OR APPLICATION NUMBER: 60/080107

APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30

APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27

FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107

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PR APPLICATION NUMBER: 60/079663

PR FILING DATE: 1998-03-27

OR APPLICATION NUMBER: 60/078910

OR FILING DATE: 1998-03-20

OR APPLICATION NUMBER: 60/078939

OR FILING DATE: 1998-03-20

OR APPLICATION NUMBER: 60/079294

OR FILING DATE: 1998-03-25

OR APPLICATION NUMBER: 60/079656

FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20

FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078936 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077791 FILING DATE: 1998-03-12

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APPLICATION NUMBER: 60/077649

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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641

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CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066
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APPLICANT: Hart, Cha
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085704
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MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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Sheppard, Paul O.
Shoemaker, Kimberly E.
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                                                                                                                                                                                                                                                                                              West, James W.
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                              Conservative
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                            Score 1851; DB 9;
Pred. No. 1.1e-160;
2; Mismatches 0;
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                                                               PRIOR
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                                                                                                                               PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/999,832A CURRENT FILING DATE: 2001-10-24
                                                                                                                                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C63
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                                                                                                PRIOR APPLICATION NUMBER: 60/064249 PRIOR FILING DATE: 1997-11-03
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                                                               APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13
               APPLICATION NUMBER: 60/077450
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                                             APPLICATION NUMBER: 60/066364
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Hillan, Kenneth J
Kljavin, Ivar J.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
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OR FILING DATE: 1998-03-11
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E: 1998-04-08
N NUMBER: 60/081203
E: 1998-04-09
N NUMBER: 60/081229
E: 1998-04-09

N NUMBER: 60/081955
E: 1998-04-15
N NUMBER: 60/081817
E: 1998-04-15
N NUMBER: 60/081819
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N NUMBER: 60/081952
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Best Local Similarity
Matches 343; Conserv
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APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLO7
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APPLICANT:
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APPLICANT: Baker Kevin P
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OR FILING DATE: 1998-05-15
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                                                            Tumas, Dan
Williams,
                                                                                     Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                            Pan, James;
Paoni, Nicholas F.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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Botstein, David
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                                                              Daniel
ms, P. Mickey
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PRIOR APPLICATION NUMBER: 60/064249 PRIOR FILING DATE: 1997-11-03 CURRENT OR APPLICATION NUMBER: 60/077791
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
OR FILING DATE: 1998-03-13
OR APPLICATION NUMBER: 60/078086
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078939
OR FILING DATE: 1998-03-20
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1998-04-15

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Sherwood, Steven
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                       Watanabe,Colin
Wood,William
                                                  Tumas, Daniel
                                                               Stewart, Timothy
                                                                              Smith, Victoria
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                                                                                                                                            Gerritsen, Mary E
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Filvaroff, Ellen
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APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29

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APPLICATION NUMBER: 60/083742 FILING DATE: 1998-04-30

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Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
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APPLICANT: Beresini, Mau
APPLICANT: Derorge, Lau
APPLICANT: Desnoyers, Lu
APPLICANT: Genyeroff, El
APPLICANT: Genyerofi, El
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 286
LENGTH: 345
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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                                           Goddard, Audrey
Godowski, Paul J
Gurney, Austin L
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Godowski, Paul J.
Gurney, Austin L.
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Wood,William
Smith, Victoria Stewart, Timothy
                              Gurney, Austin L
Sherwood, Steven
                                                                                           Gerritsen, Mary E.
                                                                                                       Gao, Wei-Qiang
                                                                                                                       Desnoyers, Luc
Filvaroff, Ellen
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o. US20030022328A1
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No. 1.1e-160;
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; LENGTH: 345
; TYPE: PRT
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US-10-123-904-286
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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APPLICANT:
APPLICANT:
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                   CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160
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mes 343; Conserv
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Gerritsen, Mary E.
                                                                                                                 Wood,William
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                                                                                                                                              Tumas, Daniel
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Filvaroff, Ellen
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File Wrapper
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SEQ ID NO 286
LENGTH: 345
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Best Local Similarity
Matches 343; Conserv
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                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/2
PRIOR APPLICATION NUMBER: 1998-12-30
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PRIOR
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CURRENT FILING DATE: 2001-0
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
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TYPE: PRT
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                                                                    APPLICATION NUMBER: FILING DATE: 1999-APPLICATION NUMBER:
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APPLICATION NUMBER: 09/
FILING DATE: 1999-02-26
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FILING DATE: 1999-09-20
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APPLICATION NUMBER:
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FILING
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2; Mismatches
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FILING DATE: 1999-APPLICATION NUMBER:

N NUMBER: 09/4/ F: 1999-12-29

09/474,071 2-29 09/474,072

FILING DATE: APPLICATION

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PRIOR APPLICATION NUMBER: 09/67;
PRIOR FILING DATE: 2000-09-30;
NUMBER OF SEQ ID NOS: 162;
SEQ ID NO 6;
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-796-753-6
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Search completed: April 29, 2003, 09:16:55 Job time: 27.5 secs
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Best Local Similarity 99.4%;
Matches 343; Conservative
                                                                                                                    OR APPLICATION NUMBER: 09/572,002
OR FILING DATE: 2000-05-14
OR APPLICATION NUMBER: 09/597,993
OR FILING DATE: 2000-06-19
OR APPLICATION NUMBER: 09/599,596
OR FILING DATE: 2000-06-22
OR APPLICATION NUMBER: 09/630,334
OR FILING DATE: 2000-07-31
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DR APPLICATION NUMBER: 09/51
DR FILING DATE: 2000-02-25
DR APPLICATION NUMBER: 09/51
DR FILING DATE: 2000-03-01
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                                                                                                                                                                                                                                                                                                                                                                                           1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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APPLICATION NUMBER: 09/606,565
APPLICATION NUMBER: 09/606,317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/665,666 FILING DATE: 2000-09-20
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                                                          VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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IMBER: 09/516,745
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Pred. No. 1.1e-160;
2; Mismatches 0;
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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1858
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                   sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_phage:*
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sp_bacteria:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	3	Length	DB	ID	Description
1	1858	100.0	345	4	Q9NRA1	Q9nral homo sapien
2	1851	99.6	345	4	Q9UL22	Q9u122 homo sapien
ω	1664	89.6	345	11	Q9QY71	mus
4	1646	88.6	345	11	Q9EQX6	6 rat
5	1635	88.0	345	11	д9ЈНV8	~
σ	1614	86.9	345	13	Q9I946	
7	741.5	39.9	370	4	Q9GZP0	Q9gzp0 homo sapien
80	740.5	39.9	364	4	Q9BWV5	Q9bwv5 homo sapien
9	737.5	39.7	370	11	Q92517	Q925i7 mus musculu
10	736	39.6	370	11	Q9EQT1	
11	645	34.7	290	11	Q9D1L8	Q9dll8 mus muscul
12	190.5	10.3	923	13	Q8QFX6	Q8qfx6 brachydanio
13	183	9.8	3623	4	060494	060494 homo sapien
14	182	9.8	691	13	057658	057658 gallus gal
15	180	9.7	34	11	Q99JM4	
16	176	9.5	977	13	091925	

Qy

1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30									21	20	19	18	17
148	148.5	148.5	149	149	151	151.5	153	153	157	•	157.5	158.5	158.5	158.5	163.5	163.5	164.5	164.5	164.5	164.5	164.5	165.5	169	171	171	171	172	176
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358	414	414	1013	1013	276	326	1019	415	1008	936	919	704	644	609	3620	921	906	906	901	901	555	926	241	1015	926	735	1012	3623
13	11	11	4	4	4	11	13	4	13	13	13	4	4	4	σ	11	4	4	4	4	4	11	11	4	4	13	11	11
057434	Q8R4W6	Q9CX06	Q9NQS4	043897	Q9BRH3	Q91ZE4	057382	Q9UKZ9	Q9DER7	Q8UVQ9	Q8UVR0	Q9H2E1	Q96IH5	096190	Q9TU53	Q9QX38	Q9H2D4	Q9H2E3	Q9H2D5	Q9H2E4	Q9H2E2	Q8QZY7	Q9Z135	Q9Y6L7	Q9UQ00	057381	Q9WVM6	070244
fuqu	Q8r4w6 mus musculu	6 mus	Q9nqs4 homo sapien	043897 homo sapien	Q9brh3 homo sapien		O57382 xenopus lae	Q9ukz9 homo sapien	Q9der7 gallus gall	Q8uvq9 gallus gall			home		a	Q9qx38 rattus norv		Q9h2e3 homo sapien	homo	homo			Ç.	Q9y617 homo sapien	r		Q9wvm6 mus musculu	070244 rattus norv

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                                      -i- SIMILARITY CONTAINS 1 CUB DOMAIN.
EMBL: AF091434: AAF00049:1; -
EMBL: AF093831: BAB03266:1; -
EMBL: AF260738: AAK51637:1; -
EMBL: AF260738: AAK51637:1; -
InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
                                                                                                                                                                                                                                                                               Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.; "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20317014; PubMed-10858496; Hamada T., U1-Tei K., Miyata Y.; "A novel gene derived from developing member of the PDGF/YEGF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                        SMART; SM00042;
SMART; SM00141;
                                                                                                                                                                                                                                           Binds to PDGF alpha and beta Receptor.";
J. Biol. Chem. 276:27406-27414(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett.
[3]
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Tsai Y.J., Lee
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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    PS01180;
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    сив;
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| growth
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MGD; MG1:163501.
InterPro; IPR000839; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; pF00431; CUB; 1.

Pfam; pF00341; PDGF; 1.

SMART; SM00042; CUB; 1.

R SMART; SM00141; PDGF; 1.

R PROSITE; PS01180; CUB; 1.

PROSITE; PS50278; PDGF_2; 1.

PROSITE; PS50278; PDGF_2; 1.
                                                                                                       Gao Z., Hart C., Piddington C., Sheppard P., Sho Gilbertson D., West J., O'Hara P.J.;
"Platelet-derived growth factor C (PDGF-C), a no binds to PDGF alpha receptor.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ da -i - SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AF117608; AAF22516.1; -.
EMBL; AF266467; AAK58566.1; -.
RGD; MGI:1859631; Pdgfc.
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Best 1
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Q9QY71;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                       Tsai Y.-J., Lee R.K.-K., Ch
"cDNA cloning of fallotein
Submitted (JAN-1999) to the
                                                                                                                                                                                                      STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mammalia; Eutheria;
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                                                                                                                                                                                                                   SEQUENCE FROM N.A:
                                                                                                                                                                                                                                                               TISSUE=OVARY;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                             Fallotein
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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Last sequence update)
Last annotation update
growth factor C).
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Pred. No. 4
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           3A58A1F701B84EA2 CRC64;
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                                                                                                                                                                                                                                                                                                       STRAIN-WISTAR; TISSUE-KIDNEY;
MEDLINE-21092670; PubMed-11162582;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.
"Molecular Cloning of SCDGF-B, a Novel Gr
SCDGF/PDGF-C/fallotein.";
Biochem. Biophys. Res. Commun. 280:733-73
-i- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AB033830; BAB19969.1; -
InterPro; IPR0000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
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01-MAR-2001 (TrEMBLrel. 16, C

01-MAR-2001 (TrEMBLrel. 16, L

01-JUN-2002 (TrEMBLrel. 21, L

Spinal cord-derived growth fa

RSCDGF.
                                                                                                                                                                                            PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 345 AA; 38734 MW;
                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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MLLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                             MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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PF00341; PDGF; 1.
; SM00042; CUB; 1.
; SM00141; PDGF; 1.
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Pred. No. 2e-149;
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Pred. No. 3
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InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organogenesis.";
Mech. Dev. 95:209-213(2000).
Mech. Dev. 95:209-213(2000).
-i-SIMILARITY: CONTAINS 1 CUB
EMBL; AF286725; AAF91483.1; -.
MGD; MGI:1859631; Pdgfc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20417814; PubMed=10960785;
Ding H., Wu X., Kim I., Tam P.P.L.,
"The mouse Pdgfc gene: dynamic expro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
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241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
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                                                                                                                GRWCGSETVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
rived growth factor C.
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                             88.0%;
                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                             Score 1635; DB 11;
Pred. No. 2.3e-148;
28; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.L., Koh G. expression
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                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                             Length
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Best Local :
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Pfam; PF00043; CUB; 1.
Pfam; PF000341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dolber.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Prohosauria; Aves; Neognathae; Galliformes; Phasianidae;
09GZP0
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WHITE LEGHORN; TISSUE-SPINAL COMEDLINE-20317014; PubMed-10858496; Hamada T. U1-Tei K. Miyata Y.; "A novel gene derived from developing member of the PDGF/VEGF family."; FEBS Lett. 475:97-102 (2000).

-I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
                                                                                                                                                                                                                                                                                              PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 345 AA; 38940 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091946
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                     VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                           VTKKYHEVLQLKPRSGVRGLHKSLTDVPLEHHEECDCVCKGNSEG
                                                                            LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                                                                                                GRWCGSSSVPSRQISKGNQIRIRFVSDEYFPSQPGFCIHYTLLVPHHTEAPSPSSLPPSA
                                                                                                                                                             GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                                                                              PREPHTYPRNTVLVWRLVAVEENVWIQLTEDEREGLEDPEDDICKYDFVEVEEPSDGTIL
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                                                                                                                                  LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                      PKFPHTYPRNTVLVWRLVAVDENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTVL
                                                                                                                                                                                                                        MLLLGLLLTSALAGRRHGAAAESDLSSKFSFPGAKEQNGVQDPQHEKIITVTSNGSIHS
                                                                                                                                                                                                                                                             289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cord-derived
                                                                                                                                                                                                                                                                    Similarity
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(TIEMBLrel. 15, Last sequence up
(TIEMBLrel. 21, Last annotation
derived growth factor.
PRELIMINARY;
                                                                                                                                                                                                                                                             Conservative
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BAB03265.1; -
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                                                                                                                                                                                                                                                                                                                                                                    CUB_domain
                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                            Pred. No. 2.3
                                                                                                                                                                                                                                                                   Score 1614; DB 13;
Pred. No. 2.3e-146;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                               97ACEA992BF5128C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORD;
370
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                                                                                                                                                                                                                                                                                                                                                                                                             spinal cords, SCDGF, is a unique
AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑĀ
                                                                                                                                                                                                                                                                              DB 13;
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RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vern RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J RA Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
CC '-- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033832; BAB18903.1; --
R EMBL; AF315316; AAG39287.1; --
R EMBL; AF335376; AAK50136.1; --
R EMBL; AF335376; AAK50136.1; --
R EMBL; AF335376; AAK50136.1; --
R EMBL; AF335376; AAK30840.1; --
R InterPro; IPR000859; CUB_domain.
R InterPro; IPR000859; CUB_domain.
R InterPro; IPR000859; TOB_boxC.
R Pfam; PF00431; CUB: 1
                                  Query Match
Best Local Si
Matches 159;
                                                                                                         PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zha Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., I Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ datal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
61-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last anotation update)
91-INAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed factor long form) (Platelet-derived growth factor D).
HSCDGF-B OR IEGF OR PDGFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21231380;
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Alitalo K., Eriksson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=IRIS; Wistow G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=AORTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J.,
"Molecular Cloning of SCDGF-B, a
SCDGF/PDGF-C/fallotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "PDGF-D is a specific,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11331881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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w
LFGLLLVTSALAGQRRGTQAESNLSSKFQFSSN---KEQNGVQD-PQHERIITVSTNGSI
                                                                                                                                                                                 PF00431; CUB; 1.
SM00042; CUB; 1.
SM00141; PDGF; 1
                                    Similarity 43.
59; Conservative
                                                                                                           PS01180; CUB; 1.
PS0278; PDGF_2; 1.
PS00430; TONE_DEPENDENT_REC_1; UNKNOWN.
370 AA; 42848 MW; D387F485E7BB7674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ressed Growth Factor (IEGF)."; (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uutela M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3:512-516(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11331882;
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Primates;
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                                      59;
                                  Score 741.5; DB 4;
Pred. No. 1.2e-62;
9; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
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a Novel
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ang J.
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                                                                      Length 370;
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B., Shimkets
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В
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL: AY027518; AAK20082.1;-
InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; PDGF; 1.
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Q9BWV5;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
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GRWCGHKEVPPRIKSRINQIKITFKSDDYFVAKPGFKIYYSL-LEDFQPAAASETNWESV
                                           GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV-----
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PS00778; PDGF_2; 1.
PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
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Pred. No. 1.
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01-DEC-2001
01-JUN-2002
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SMART; SW00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
PROSITE; PS50278; PDGF_2; 1.
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MEDLINE=21231380; PubMed=11331882;
LAROCHALLE W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Glese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Ver
Glese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Ver
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
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EMBL: AF335583; AAK38839.1; -.
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InterPro; IPR000072; PD_growth_factor.
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                          VVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEC
                                                                                                                                                                                                                             QISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV----
                                                                                                                                                                                                                                                                                                                            WRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                ORRGTQAESNLSSKFQFSSNKEQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPR
                                                                                              ITDPT-LTADALDKTVAEFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK
                                                                                                                            ITSRTNQIKITFKSDDYFVAKPGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPS
                                                                                                                                                                                                                                                                                                       WWLRS
                                                                                                                                                                                                                                                                                                                                                                                                      QRASIKALRNANLR-----RDESNHLTDLYQREENIQVTSNGHVQSPRFPNSYPRNLLLT
- VDLDRLNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSC
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                                                                                                                                                                                                                                                                                                  -QEKTRIQLSFDHQFGLEEAENDICRYDFVEVEEVSESSTVVRGRWCGHKEIPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; S
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(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 21, Last annotation
rived growth factor D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 737.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.8e-62;
9; Mismatches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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**MEDITME=21092670; PubMed=11162582;

**MEDITME=21092670; PubMed=11162582;

**Melecular Cloning of SCDGF-B, a Novel Growth Factor Home Molecular Cloning of SCDGF-B, a Novel Growth Factor Home SCDGF/PDGF-C/fallotein.";

**SCDGF/PDGF-C/fallotein.";

**SCDGF/PDGF-C/fallotein.";

**BOCCHEM. Biophys. Res. Commun. 280:733-737(2001).

**BIOCHEM. Biophys. Res. Commun. 280:733-737(2001).

**COMMINIARITY: COUTAINS 1 CUB DOMAIN.

**REMBL; AB052170; BAB18920.1; -...

**REMBL; AB052170; BAB18920.1; -...

**InterPro; IPR000072; PD_growth_factor.
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Best Local
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SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 370 AA; 42809 MW;
   Q9D1L8;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EQT1;
01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                  Q9D1L8
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Mammalia; Eutheria;
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RSCDGF-B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                SVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTLNWKSCTCSSGKTVKKYHEVLKFEPGH
                                                                                                                                                                                                                                 SVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---
                                                                                                                                                                                                                                                                                           LEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNF:|||::| | || | | ::|: ||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                       LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC
                                                                                                                                                  FKRRGKAKNMALVDIQLDHHERCDCIC
                                                                                                                                                                                -KTGVRGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                            VEDLLKYFNPASWQDDLENLYMDTPRYRGRSY-HERKSK-VDLDRLNDDVKRYSCTPRNH
                                                                                                                                                                                                                                                                                                                                        PGFKIYYSFVEDFQPEAASEINWESVTSSFSGVSYHSPSVM-DSTLTADALDKATAEFDT
                                                                                                                                                                                                                                                                                                                                                                           PGFCIHYNIV---MPQFTEAV-----SPSVLPPSALPLDLLNNAITAFST
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149; Conserv
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
derived growth factor-R
                                   (TrEMBLrel.
   (TrEMBLrel.
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                                                                  PRELIMINARY;
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Rodentia;
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Pred. No. 3
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   sequence update) annotation updat
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenpush V. Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T. Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Q8QFX6
Q8QFX6;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SHOULD CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono B., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDFGD OR 111000.
Mus musculus (Mouse).
Mus mvota; Metazoa; Chordata;
heria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 (EMBL; AK003359; BAB22735.1; MGD; MGI:1919035; Pdfgd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
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PDFGD OR 1110003I09RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                243 TVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                       EENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGN 138
                                                                                                                                                              VTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                              LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                                                                                                                                                                                                       LNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCTCSSGK
                                                                                                                                                                                                                                                            LTADALDKTVAEFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK-VDLDR
                                                                                                                                                                                                                                                                                                                         QIKITFKSDDYFVAKPGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPSITDPT- 124
                                                                                                                                                                                                                                                                                                                                                         QIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
 (TrEMBLrel.
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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45.4%;
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 21,
21,
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 Last
                Created)
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Pred. No. 1.5e-53;
8; Mismatches 80;
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                                                   PRT;
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 sequence update)
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mouse cDNA collection.";

Storch K.-F.,

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Length 290; Indels

26;

Gaps

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SPSVLPPSA 180

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242

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Query Match
Best Local :
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060494, Q96RU9;
01-AUG-1998 (TIEMBLICEL 07,
01-JAN-1999 (TIEMBLICEL 09,
01-JUN-2002 (TIEMBLICEL 21,
                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-97476251; PubMed-9334227;

Birn H., Verroust P.J., Nexo E., Hager H., Jacobsen C.,

Christensen E.I., Moestrup S.K.;

"Characterization of an epithelial approximately 460-kDa protein that facilitates endocytosis of intrinsic factor-vitamin B12 and binds receptor-associated protein.";

J., Biol. Chem. 272:26497-26504(1997).
Aminoff M., "The genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbi "Neuropilin-1 is required for normal vascular development mediator of VEGF-dependent angiogenesis in zebrafish."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY064213; AAL40862.1; ...
SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                "The human intrinsic factor-vitamin B12 receptor, cubilin: m characterization and chromosomal mapping of the gene to 10p autosomal recessive megaloblastic anemia (McA1) region.";
                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98241400; PubMed-9572993;
MCDLINE-98241400; PubMed-9572993;
MCDLINE-98241400; PubMed-9572993;
MCDLINE-98241400; PubMed-9572993;
MCDLINE-99241400; PubMed-99241400;
MCDLINE-99241400; PubMed
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intrinsic
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   genomic
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                                                                    91:3593-3600(1998).
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   130-3623 FROM N.A.
Brady S., Verroust
c structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                              PubMed=9572993;
tiansen M., Silahtaroglu A., Hansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; 27.6%;
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   Verroust
e of the h
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Last sequence update)
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Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
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   human
                    P.J.,
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   CUBN
 Moestrup
CUBN gene
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encoding
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                    Receptor;
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Pfam;
                                                                              PROSITE: PS00010; ASX_HYDROXYL; 4.
PROSITE: PS00180; CUB; 27.
PROSITE: PS00022; EGF_1; UNKNOWN_4.
PROSITE: PS01186; EGF_2; UNKNOWN_2.
PROSITE: PS01187; EGF_CA; 3.
Calcium-binding; EGF-like domain; G
                                                                                                                                                                                SMART; SM00042; CUB; 26.
SMART; SM00179; EGF_CA; 3.
SMART; SM00001; EGF_like;
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InterPro;
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EMBL;
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                                                                  Repeat; Signal.
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IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR000742; EGF_2.
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; EGF; 5.
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                    398991 MW;
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                                POTENTIAL.
INTRINSIC FACTOR-B12
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                                                                                Glycoprotein;
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Best Local S
         SMART; SM00042; SMART; SM00179; SMART; SM00235;
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01-JUN-1998
01-JUN-2002
                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=20267865; PubMed=10806368;

Reynolds S.D., Zhang D., Puzas J.E.,

Reynolds P.R.;

"Cloning of the chick BMP1/Tolloid cl
                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1212
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          PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 3.
SMART; SM00179; EGF_CA; 1.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                        tissues.";
Gene 248:233-243(2000)
PROSITE;
                                                                                                                                                InterPro;
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                                                                                                                                                                       EMBL; U75331; AAC02259.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Gallus.
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                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                    Bone morphogenetic
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PF00431; CUB; 3.
PF00008; EGF; 1.
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PS00010;
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IPR000859;
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ASX_HYDROXYL;
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Neognathae; Galliformes; Phasianidae; Phasiani
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EGF-like.
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Pred. No. 8.6e-08;
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Best Local
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Q99JM4;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                       ADGFC.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Calcium-binding; EGF-11ke domain; Glycoprot
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similar to
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                                                                                                                                                                                                              SEQUENCE
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NON_TER 1 1
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1 RPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
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                                                                                                                                                                                                              34 AA;
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                                                                                                          Conservative
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growth factor, C polypeptide
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                                                                                                    Score 180; DB 11;
Pred. No. 3.3e-10;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 182; DB 13;
Pred. No. 1.2e-08;
0; Mismatches 48;
                                                                                                                                                                                                              F4AB6A3A414AED9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                     Length
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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QУ	Qy Db	Db Db	Qy Db	Qy Db Qy	Query Best : Match	RESULT 1 JC7591 spinal cc C; Speciae C; Date: 2 C; Access R; Hamada Biochem. A; Title: A; Referer A; Access A; Molecul A; Residue A; Gene: 5 C;		
335 CDCVC 339	278 KRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE :	183 WESVTSSISGVSYNSPSVTDPT-LIADALDKKIAEFDTVEDLLKYFNPESWQEDLENNYL 218 PTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGGLLV	119ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV	3 LFGLLLVTSALAGÓRRGTQAESNLSSKFQFSSNKEQNGVQD-PQHERIITVSTNGSI	Match 40.0%; Score 742.5; D Local Similarity 43.6%; Pred. No. 9.5e- es 159; Conservative 59; Mismatches	ord-derived growth factor-B precursor - 1: Homo sapiens (man) 10-Jun-2001 #sequence_revision 30-Jun-200 10-Jun-2001 #sequence_revision 30-Jun-200 10-Jun-2001 #sequence_revision 30-Jun-200 10-Jun-2001 #sequence_revision 30-Jun-200 10-Jun-2001	ALIGNMENTS	30 118.5 6.4 276 2 A47290 31 114.5 6.2 148 2 D49530 32 114.5 6.2 241 1 PFHUG2 33 112.5 6.1 215 2 S08220 34 112.5 6.1 215 2 S08220 35 111.5 6.1 226 2 I51550 36 111.5 5.9 2403 2 A59386 37 110.5 5.9 2403 2 A59386 38 110 5.9 166 2 JN0248 39 109 5.9 197 2 S25096 40 108.5 5.8 226 1 TVMVSS 41 108 5.8 226 1 TVMVSS 41 104 5.6 232 2 A41551 42 104.5 5.6 232 2 A41551 43 104 5.6 231 1 PFHUG1 44 104 5.6 211 1 PFHUG1 45 103 5.5 770 2 D89447
	KTGVRGLHKSLTDVALEHHEE 334 : : : KRRGRAKTMALVDIQLDHHER 359	EDLLKYFNPESWQEDLENMYL 241 VSIREELKRIDTIFWPGCLLV 277 : : : : VNIREELKLANVVFFPRCLLV 299	PCIHYNIVMPQETEAV 171 : :::	NLSSKFQFSSNKEQNGVQD-PQHERIITVSTNGSI 58	B 2; Length 370; 57; 114; Indels 33; Gaps 10;	human 01 #text_change 24-Aug-2001 1 rowth factor homologous to SCDGF/PDGF 11162582 predicted <sig> ttor-B #status predicted <mat> growth factor/vascular endothelial g</mat></sig>		TSG-6 homolog PS4 16K vascular endot platelet-derived g platelet-derived g platelet-derived g platelet-derived g yus.2 protein - Af sanko - human platelet-derived g vascular endotheli platelet-derived g protein F57C12.1 [

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intrinsic factor-B12 receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence
C;Accession: T09456
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                A;Cross-references:
C;Genetics:
A;Map
                                                A; Molecule type: mRNA
A; Residues: 1-3623 <K
                                                                                                   A; Reference number: A; Accession: T09456
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Blood 91, 35
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F;1-17/Domain:
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A; Residues: 1-370 <HAM>
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                                                                                    preliminary; translated
                                                                                                                                                                         i, R.; Kristiansen, M.; Silahtaroglu, 3593-3600, 1998
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                                                                                                                     Z16677;
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cord-derived growth factor-B #status
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                                                                                                                     MUID:98241400;
                                                                                                                                                     factor-vitamin B12 receptor,
                                                                                                                                                                                                                                                            Cubilin precursor -
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Pred. No. 3
                                                                                    from
                                  NID:g3929528;
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3.5e-56;
1es 93;
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                                                                                                                                                                                         A.; Hansen,
                                  PIDN: AAC82612.1;
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A;Gene: GDB:BMP1

A;Cross-references: GDB:125203; OMIM:112264

A;Cross-references: GDB:125203; OMIM:112264

A;Map position: 8p21-8p21

C;Function:

A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen to the control of the carboxyl-terminal propeptide of collagen to the control of the carboxyl-terminal propeptide of collagen to the control of the carboxyl-terminal propeptide of collagen to the control of the carboxyl-terminal propeptide to the control of the carboxyl-terminal propeptide to the control of the carboxyl-terminal propeptide of collagen to the control of the carboxyl-terminal propeptide of calcium; duplication; figure for the carboxyl-terminal propeptide of carbo
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C;Genetics:
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A; Reference number: A37278;
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N;Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens (man)
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A; Residues: 1-730 <WOZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYPHGINCTWHIL-VQPNHLIHLMF-ETFHLEFHYN--CTNDYLEVYDTDSETSLGRYCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:M22488; NID:g179499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of bone
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26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celeste,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone formation: molecular clones and
MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LY--SCTPRNFSVSIREELK-RTDTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -YPNNW----ECIYRITVRTGQLIAVHFTNFSLEEAI 1099
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Pred. No. 8.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 А.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:AAA51833.1;
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                                                                                                                                                                                                                                                                                                                      duplication;
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A.Experimental source: tadpole, brain
A:Experimental source: tadpole, brain
A:Note: this protein has motifs homologous to complement components Clr and Cls and to C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal recision of the components of the neuronal recision of the component of the neuronal recision of the component of the neuronal recision of the neuro
   Neuron 7, 295-307, 295-307, A;Title: The A5 antigen, a c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 IKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE---CKYDYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 NGSIHSPREPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                     ----QFTEA--VSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
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                                                                                                                                                                                                                                                                                                                                                       ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFAPKMQEIV--LEFESFELEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor - African clawed frog
Xenopus laevis (African clawed
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37.3%;
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31.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
Ong,
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Pred. No. 2.9
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Pred. No. 1.5e-07;
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                                                                           20-Aug-1994 #text_change
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Kung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; DB 1;
2.9e-07;
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A;Gene: CUBILIN
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status pro
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A; Title: The intrinsic factor-vitamin B12 receptor and target A; Reference number: Z16459; MUID:98148073; PMID:9478979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-3623 < MOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T08618
R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;398-510/Region: complement 1r/1s-like repeat F;398-507/Domain: C1r/C1s repeat homology <C1R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;285-394/Domain: C1r/C1s repeat homology <C1R
                                                                                                                                                                                                                                                                                                                                                  F;133-164/Domain:
F;436-467/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intrinsic factor-B12 receptor CUBILIN precursor
C; Species: Rattus norvegicus (Norway rat)
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A; Residues: 1-707 < MAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Cloning
                                                                                                                                                                                                                                                  Matches
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Best Local S
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                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                            2 SLFGLLLVT--SALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIH 59
LGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY-----NIVMPQFTEAVSP 173
                                                                                            SPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTI 119
                                              SPGHPNVYPRGVNCTWHVV-VQRGQLIRLEFSS-FYLEFHYN--CTNDYLEIYDTAAQTF
                                                                                                                                             SVYNILYVTFVKSSSMENRGFTA-----KFSSDKLECG-----EVLTAST-GIIE
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EGF homology <EGF1>
EGF homology <EGF>
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Pred. No. 3
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A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type (;Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cls repeat homology; E C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl F:1-22/Domain: signal sequence #status predicted <SIG> F;23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT> F;33-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT> F;130-321/Domain: clr/Cls repeat homology <CIR1> F;33-544/Domain: Clr/Cls repeat homology <CIR1> F;435-544/Domain: Clr/Cls repeat homology <CIR2> F:551-587/Domain: Clr/Cls repeat homology <CIR2>
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A;Title: Bone morphogenetic protein-1 and a mammalian toll A;Reference number: A58788; MUID:95096114; PMID:7798260
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Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                            ;551-587/Domain: EGF homology <EGF>
;591-700/Domain: EGF homology <CIR3>
;591-700/Domain: CIr/Cls repeat homology <CIR3>
;738-752/Region: histidine-rich
;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
;91,142,332,363,599/Binding site: zinc (His, His, Tyr) #status predicted
;213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Map position: 8p21-8p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:125203; OMIM:112264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA
;Residues: 703-823 <TAK>
;Cross-references: GB:L35278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rocollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form Alternate names: bone morphogenic protein splice form BMP-1/His species: Homo saplens (man) species: Homo saplens (man) the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
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                                                                                        NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTDVALEHHEEC
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                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                  site:
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                                                                                                                                                                                     19;
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                                                                                                                                                                                                                           Score 173;
Pred. No. 9.
                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                           DB 1;
.3e-07;
                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                            Gaps
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A; RCCCSSAV...

A; NOICCULE type: mRNA
A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A; CROSS-Teferences: GB: M2248], NID: 9179499; PIDN: AAA51833.1;
R; Takahara, K.; Lyons, G.E.; Greenspan, D.S.
R; Takahara, K.; Lyons, G.E.; Greenspan, D.S.
T Riol. Chem. 269, 32572-32578, 1994
                                                                                                                                                                                                                                                                                                                                                  F;33-986/Product: procollagen C-endopeptidase tolloid-like splice form #status pred F;33-986/Product: procollagen C-endopeptidase tolloid-like splice form #status pred F;33-321/Domain: clr/cls repeat homology <cIR1>
F;32-431/Domain: Clr/cls repeat homology <cIR2>
F;435-544/Domain: Clr/cls repeat homology <cIR3>
F;591-790/Domain: EGF homology <EGIV
F;591-700/Domain: EGF homology <EGIV
F;707-742/Domain: Clr/cls repeat homology <cIR4>
F;707-742/Domain: Clr/cls repeat homology <cIR4>
F;707-742/Domain: Clr/cls repeat homology <cIR4>
F;707-7456/Domain: Clr/cls repeat homology <cIR4>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted F;1142,312,183,752-318,375-397,435-461,488-510,551-563,559-572,574-587,591-617,6 F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted F;114Active site: Glu #status predicted F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes hydrotysis of the current of Superfamily; procollagen C-endopeptidase; astacin homolo C; Keywords: alternative splicing; beta-hydroxyasparagine; F;1-22/Domain: signal sequence #status predicted <SIC>
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A; Map position: 8p21-8p21
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A; Residues: 703-986 <TAK>
A; Cross-references: GB:L35279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Bone morphogenetic protein-1 and a mammalian t A; Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Wozney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A37278; B58788 R; Wozney, J.M.; Rosen, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             procollagen C-endopeptidase (EC 3.4. N,Alternate names: bone morphogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Novel regulators of bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                           Matches
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654
                                                                                                                    599
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                                                                                                                                                      55 NGSIHSPREPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF
                                                        --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG ----NDVCKYDFVEVRS
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lators of bone formation: molecular A37278; MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                 9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celeste,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID: g619860;
                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                 Pred. No. 2.007; Mismatches
                                                                                                                                                                                                                                                                    Score 169; DB 1;
Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.J.; Mitsock, L.M.; Whitters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: AAC41710.1;
                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                Length 986
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I49540 procollagen C; Species:

Mus musculus (house

(EC 3.4.2 use mouse)

3.4.24.19)

precursor,

tolloid-like

splice

gnom

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A; Gene: Bmp-1
C; Superfamily:
C; Keywords: h
                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:PCOLCE
A;Cross-references: GDB:305468; OMIM:600270
A;Map position: 7q21.3-7q22
C;Superfamily: Clr/Cls repeat homology
C;Keywords: extracellular protein; glycoprot
F;1-25/Domain: signal sequence #statumence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision
C:Accession: A55362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:135-526/Domain: astacin homology <AST>
F;556-592/Domain: EGF homology <EG1>
F;556-705/Domain: C1r/C1s repeat homology <C1R>
F;712-747/Domain: EGF homology <EG2>
F;218,222,228,277/Binding site: zinc (His, His, His, F;218,222,228,277/Binding site: zinc (His, His, His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Sh
J. Biol. Chem. 269, 26280-26285, 1994
A;Title: Type I proclagen COOH-terminal proteinase enhancer protein: identification,
A;Reference number: A55362; MUID:95014462; PMID:7523404
A;Accession: A55362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: I49540
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CfSpecies: H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-991 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: hydrolase; metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Genetics:
                                                                                                                                                                                                                              Reywords: extracellular protein; glycoprotein; pyro:1-25/Domain: signal sequence #status predicted <SIG:26-449/Product: #status predicted <MATP:37-146/Domain: Clr/Cls repeat homology <CLR>:37-146/Domain: Clr/Cls repeat homology <CLR>:27/Domain: Clr/Cls repeat homology <Clr>:28/Modified site: pyrrolidone carboxylic acid (Gln):29/431/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
Residues: 1-449 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: not compared with conceptual
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Best Local
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                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604
                                                               168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 -- PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                       Local Similarity
                                                                                   GSIHSPRFPHT-YPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEV--- 111
                   EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFT---
                                                               GTLTTPNWPESDYPPGISCSWHIIAPPDQV-IALTF-EKFDLE--PDTYCRYDSVSVFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG-----NDVCKYDFVEVRS 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I C-proteinase enhancer protein precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:L33799; NID:g642907;
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                                                                                                                                                                       33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                 22;
Score 169; DB 2;
Pred. No. 2.6e-06;
7; Mismatches 39
                                                                                                                                                                       Score 154; DB 2;
Pred. No. 1.9e-05;
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAA61949.1;
                                                                                                                                                                                                                                                      (Gln) (in mature
                                                                                                                                                                                                                                                                                                                                         pyroglutamic
<SIG>
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                                                                                                                                                                                      Length 449
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                                       A; Note:
C; Geneti
                                                                                                                                                                                                   A;Reference number: A59271; MUID:97242412; PMID:9087411 A;Accession: A59271
                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C;Accession: A59271
C;Accession: William T. Stover. C.M.; Schwaeble, W.J.; Laursen, S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                 R;Thiel, S.; Vorup-Jensen, T.;
Nature 386, 506-510, 1997
A;Title: A second serine protea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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                                                                                                     A;Cross-references: GB:Y09926; NID:g4007626; A;Experimental source: tissue liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: A39288
                                                                                   A; Note: submitted to GenBank,
                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                        A; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: FlyBase:tld
  A; Cross-references:
                                                                                                                                              A; Residues: 1-686 <JEN>
                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: mannose binding
                                                                                                                                                                                                                                                                                                                                                                                                     Ra-reactive factor (EC 3.4.21.-) 2 precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                             A59271
                                           Geneti
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Best Local
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                     GDB:MASP2
                                                             parts of this sequence,
  GDB:6071500
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December 1996

PIDN:CAA71059.1;

PID: 94007627

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S.B.;

Poulsen

protein-associated serine proteinase 2 (MASP-2)

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the mature protein,

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dorsal ventral patterning protein tolloid (EC 3.4.2 c;Species: Drosophila melanogaster C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: A39288
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0003719
C;Superfamily: dorsal-ventral patterning protein tolloid; a:C;Superfamily: dorsal-ventral patterning protein tolloid; a:C;Seywords: duplication; hydrolase; metalloproteinase; zinc F;136-329/Domain: astacin homology <AST>
F;352-464/Domain: Clr/Cls repeat homology <ClR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Shimell, M.J.; Ferguson, E.L.; Childs, Cell 67, 469-481, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вb
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F;585-620/Domain: EGF homology <EG1>
F;624-740/Domain: Clr/Cls repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1057 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The Drosophila
                                                                                                                                                                                                                                                                                             747-782/Domain: EGF homology <EG2>
787-895/Domain: Clr/Cls repeat homology <C1R4>
900-1013/Domain: Clr/Cls repeat homology <C1R5>
221,225,231,280/Binding site: zinc (His, His, His,
                                                                                                                                                                                                                                                                          222/Active site: Glu #status predicted
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                                                                                        472 LKLTKDQSIDSPNYPMDYMPDKECVWRITA-PDNHQVALKF-QSFELE--KHDGCAYDFV
                                          EVEE -- PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 147
                                                                                                                                  ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGPGPKRGTEPKVKLPPKSQP 302
EIRDGNHSDSRLIGRFCGDKLPPNIK-TRSNQMYIRFVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKE
                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dorsal-ventral patterning gene tolloid 288; MUID:92034970; PMID:1840509
                                                                                                                                                                                                     8.0%;
                                                                                                                                                                                20;
                                                                                                                                                                                Score 148.5; DB 1;
Pred. No. 0.00017;
0; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EC 3.4.24.-) - fruit
                                                                                                                                                                                                                                                                                                                                                                                            <C1R3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; F;1-15/Domain: signal sequence #status predicted <STG>
F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: Clr/Cls repeat homology <ClR1>
F;19-134/Domain: EGF homology <CGR2>
F;184-293/Domain: Clr/Cls repeat homology <CIR2>
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J. Neurosci. 17, 755-764, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 22-Oct-1999
C; Accession: T31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: probable metalloprotease TBL-1
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tolloid-BMP-1 like protein 1 - California sea hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Molecule type: mRNA
;Residues: 1-1070 <LIU>
;Cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC47485.1
;Cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC47485.1
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72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,72-90,142-165,167-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180,182-180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL---TFDERFGLEDPEDDICKYDFVEVE 112
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CACCLHNCN-----ECQC
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                                                                NKER-----LQGQYCGFMAPPSITSLSNELRIEFRSDDTLQKTGFSMDYVADVDECASS
                                                                                                                                                                                                                                                                     LPPSALPLDLLNNAITAFS-----TLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFG
                                                                                                                                                                                                                                                                                                                                         DHGCEHVCVNTLGSYECTCKIGYELHSDGKKCEKACGGYLDAPSGTISSPSF-----PDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFLNSPAYPDEYGSDKVCEW-VITVREGYQVALEFATFETEF---DPD---CAYDYVEIR 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 139.5; DB Pred. No. 0.0011;
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Pred. No. 0.00027;
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A;Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2 C;Superfamily: Clr/Cls repeat homology; astacin homology C;Keywords: hydrolase; metalloproteinase; zinc F;L-19/Domain: signal sequence #status predicted <SIG>F;20-597/Product: metalloproteinase 10, blastula #status F;202-295/Domain: astacin homology <AST>F;303-445/Domain: Clr/Cls repeat homology <CIRl>F;484-592/Domain: Clr/Cls repeat homology <CIRl>F;484-592/Domain: Clr/Cls repeat homology <CIRl>F;190,194,200/Binding site: zinc (His) #status predicted
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A;Title: Structure of the gene encoding the sea urchin the Reference number: S71352; MUID:96300240; PMID:8706676
A;Accession: S71352
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                                                                                                                                                                                                                                                                                                                    δÃ
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A:Residues: 1-7,'S',9-10,'V',12-28,'H',30-72,'D',74-77,'SK',
9-571,'N',573-584,'D',586-595,'D',597 <LEP>
A;Cross-references: EMBL:X56224; NID:g10928; PID:g10929
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:99979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: gene tolloid protein homolog
C;Species: Paracentrotus lividus (common urchin)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998
C;Accession: $71352; A44880; $22060
R;Lhomond, G.; Ghiglione, C.; Lepage, T.; Gache, C.
Search completed: April 29, Job time: 20.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A44880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development 114, 147-163, 1992 A; Title: Spatial and temporal expression pattern during
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Gapop 10.0 ,
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     MSLFGLLLVTSALAGQRRGT.....DVALEHHEECDCVCRGSTGG
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TLD_DROME
VEGD_HUMAN
MAS2_HUMAN
VEGD_MOUSE
BP10_PARLI
CRAR_MOUSE
  PCO1_RAT
PDGA_RABIT
VEGC_MOUSE
TSG6_HUMAN
PDGB_FELCA
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homo sapien
gallus gall
homo sapien
drosophila
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royctolagus
mus musculu
homo sapien
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SMART; SM00231; FA58C; 2. SMART; SM00137; MAM; 1. PROSITE; PS00740; MAM_1; 1.
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ALIGNMENTS

RESULT	YENLA
35	NRP1_XENLA STANDARD; PRT; 928 AA.
T C	(Rel.
3 5	1. 24, Last
DE .	Neuropilin-1 precursor (A5 protein) (A5 antigen).
SO	Xenopus laevis (African clawed frog).
88	
2 2	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae: Xenopus
8 8	NCBI_TaxID=8355;
RN	[1]
7	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
2 2	9
RT.	"The A5 antigen, a candidate for the neuronal recognition molecule.
감	has homologies to complement components and coagulation factors.";
3 2	TREATED TO THE TREATED TO THE TREATED TO THE TREATED OF THE
<u>ය</u> :	CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
38	CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
င္ပ	SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION
88	BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.
2 2	- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISITAL CENTER
8	NEURONS.
8	- SIMILARITY: BELONGS TO
38	-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
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88	This SWISS-PROT entry is copyright. It is produced through a collaboration
3 6	between the Swiss Institute of Bioinformatics and the EMBL outstation -
88	use by non-profit institutions as long as its content is in no way
റ്റ	by and for commer
36	7
3 6	or send an email to licenseelsp-sib.ch).
DR	EMBL; D10467; BAA01260.1;
DR	HSSP; P12259; 1CZT.
ק ק	InterPro: IPR000859; CUB_domain.
DR:	IPR000998;
DR	0431; CUB; 2
DR	PF00629; MAM; 1.
בל ק	PRINTS: PROGOCO: MANDOMAIN
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Best Local Similarity
MEDLINE-94085787; PubMed-8262384; MEDLINE-94085787; PubMed-8262384; Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.; Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.; Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.; Menon M., Xue Y., Wood T.I., Ong R.C., Kung H.F.; Sone morphogenetic protein-1 during early embryonic development."; Gene 134:257-261(1993).

-i- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LAD DIFFERENTIATION OF DEVELOPING ORGANS.

-i- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTFI-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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                                                                                                                                                                                                                  TISSUE=Embryo;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                            Xenopodinae;
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PS01286;
PS50060;
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Pred. No. 1.4e-07;
9; Mismatches 73;
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EXTRACELLULAR (POTENTIAL).
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PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS000021; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
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SMART; SM00042; CUB; 3.
SMART; SM00179; EGF_CA; 1
SMART; SM00235; ZnMC; 1.
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                                                                                                                                                                     SEQUENCE
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the European Bioinformatics Institute
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MEROPS; M12.0
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                                                  LTSDSKLHGKFCGS-ELPAVITSQYNNMRIEFKSDNTV-SKKGF
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SM00179; EGF_CA; 1.
SM00235; ZNMC; 1.
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IPR000130;
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e; EGF-like domain; Zinc; Calcium; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrict use by non-profit institutions as ion as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MEDLINE=92315921; PubMed=1618141;
Reynolds S.D., Angerer L.M., Palis J., Na
"Early mRNAs, spatially restricted along
                                                                                  METAL
ACT_S
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG
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HSSP; P28825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus.
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                                                               METAL
                                                                                                      DOMAIN
                                                                                                                 DOMAIN
                                                                                                                          DOMAIN
                                                                                                                                     DOMAIN
                                                                                                                                                                                                  Metalloprotease
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InterPro; IPR000859; CUB_doma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: ASYMME OF THE BLASTULA.
DEVELOPMENTAL STAGE: VERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BMP-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND HATCHING)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                            PR00480; ASTACIN.
                                                                                                                                                                                                                                                   PS00142; ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                          IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR000130; Zn_MTpeptdse.
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; Echinodermata; Eleutherozoa; Echinozoa;
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Last annotation update)
r (EC 3.4.24.-).
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  9.3%;
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ZINC (CATALYTIC)
ZINC (CATALYTIC)
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                                                            SIMILARITY).
SIMILARITY).
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Length
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          Best Local Similarity
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Takahara K., Lyons G.E., Greenspan D.S.;
"Bone morphogenetic protein-1 and a mammalian tolloid homologue are encoded by alternatively spliced transcripts which are differentially expressed in some tissues.";
J. Biol. Chem. 269:32572-32578(1994).
                                                                                                                                                                                      Janitz M., Heiser V., Boettcher U., La
"Three alternatively spliced variants
bone morphogenetic protein-1.";
J. Mol. Med. 76:141-146(1998).
                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=98160316; PubMed=9500680;
                                                                                                                                                                                                                                                                                                                                                                                                                Wozney J.M., Rosen V., Celeste A.J., Kriz R.W., Hewick R.M., Wang E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM BMP1-1).
MEDLINE=89072730; PubMed=3201241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is identical to the protein protein-1.";
                                                                                                         MEDLINE=95096114; PubMed=7798260;
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Pfam; PF004031; CUB; 5.

Pfam; PF01400; ASTACIN; 1.

PRINTS; PR00480; ASTACIN.

SMART; SM00142; CUB; 5.

SMART; SM00235; ZNMC; 1.

PROSITE; PS001142; ZINC_PROTEASE; 1.

PROSITE; PS011180; CUB; 5.

PROSITE; PS011180; CUB; 5.

PROSITE; PS011180; CUB; 5.

PROSITE; PS0117; EGF_1; FALSE_NEG.

PROSITE; PS0117; EGF_1; PALSE_NEG.

PROSITE; PS01186; EGF_1; FALSE_NEG.

PROSITE; PS01186; EGF_1; PALSE_NEG.

PROSITE; PS01186; EGF_1; PALSE_NEG.
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EMBL; W22488; AAA51833.1; -.
EMBL; Y08723; CAA69973.1; -.
EMBL; Y08724; CAA69974.1; -.
EMBL; Y08725; CAA69975.1; -.
EMBL; L35278; AAC41703.1; -.
EMBL; L35279; AAC41710.1; -.
PIR; A37278; A37278.
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InterPro; IPR000152; A
InterPro; IPR000859; C
InterPro; IPR000561; E
InterPro; IPR001881; E
InterPro; IPR000130; Z
                                                                                                                                                                                                                                                                  Glycoprotein;
SIGNAL
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METAL
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M12.005; -.
Genew; HGNC:1067; BMP1.
MIM; 112264; -.
                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative splicing.
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO PEPTIDASE FA
SIMILARITY: CONTAINS 2 EGF-LIKE DOW
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: ACTIVITY IS IN ENDOPEPTIDASE ENHANCER PROTEIN. ALTERNATIVE PRODUCTS: 7 isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: BINDS 1 ZINC ION (BY ENZYME REGULATION: ACTIVITY IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND II. INDUCES CARTILAG
CATALYTIC ACTIVITY: Clea
Ala-|-Asp in type I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   here), BMP1-4,
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                                                                                                                                                                                                                                                                                                                                                 Cytokine; Repeat; Bone; Cartilage;
                                                                                                                                                                                                                                                                                                                            EGF-like domain; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMP1-5, BMP1-6 and
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CUB_domain.
EGF-like.
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ZINC (CATALYTIC)
ZINC (CATALYTIC)
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EGF-LIKE CUB 4.
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BMP1-7;
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                                                                                                                         CALCIUM-BINDING
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                                   Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                      BMP1_MOUSE STANDARD; PRT; 991 AA. P98063; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Bone morphogenetic protein 1 precursor (EC 3. (Procollagen C-proteinase) (PCP) (Mammalian to
                                                                                                                                                                                                                                                                                       MOUSE
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OF SIMILARITY.
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17; Mismatches
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VLEGAGDRHISHLSGLELLLCPHALVDTVRAPSAHAGD

THAHTHTHYHTHCPIAGETGRFPLGASRLSPOGPGHLTLA
PQEGSYLDFWDTHRGDPKPRRRKSLKTFSLTPATFRGIWA
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IVPKYEVNGVKFPIGQR -> VLHSSLLLLSGGSRNGASFP
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AACGGFLTKLNGSITSPGWPKEYPPNKNCIWQLV
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                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
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(IN ISOFORM BMP1-6)
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(IN ISOFORM BMP1-5)
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Metalloprotease; EGF-like domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB; 5. Pfam; PF01400; Astacin; 1.
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HSSP; P00736; 1APQ.
MEROPS; M12.005; -.
MGD; MGI:88176; Bmp1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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InterPro; IPR000152; Asx. hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000130; Zn_MTpeptdse.
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MEDLINE=94229342; PubMed=8174772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.; 
Embryonic expression of mouse bone morphogenetic 
which is related to the Drosophila dorsoventral ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENDOPEPTIDASE ENHANCER PROTEIN.

TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF I OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A. SIMILARITY: CONTAINS 2 EGF-LIKE DOWAINS.

SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CLEAVES THE C-TERMINAL PROPERTIDES OF AND II. INDUCES CARTILAGE AND BONE FORMATION. CATALYTIC ACTIVITY: Cleavage of the C-terminal Ala-|-Asp in type I and II procollagens and at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: BINDS 1 Z
ENZYME REGULATION:
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                                                                                                                                                                                                                                                                                                                                                                                    ; PS00142; ZINC_P
; PS01180; CUB; 5
; PS00100; ASVH_1;
; PS00002; EGF_1;
; PS01186; EGF_2;
; PS01187; EGF_CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long
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GULATION: ACTIVITY IS INCREASED BY THE
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EGF_1; FALSE_NEG.
EGF_2; 2.
EGF_CA; 2.
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Best Local
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
form of vascular endothelial growth factor (VEGF) and of placenta
growth factor-2, but only neuropilin-2 functions as a receptor for
the 145-amino acid form of VEGF.",
J. Biol. Chem. 275:18040-18045(2000).
J. Biol. Chem. 275:18040-18045(2000).
-i- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-16
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
-i- SUBBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                  MEDLINE=98188099; PubMed=9529250; Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun "Neuropilin-1 is expressed by endothelial and tumor cells isoform-specific receptor for vascular endothelial growth Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRP2_HUMAN
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                            CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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lin-2, a novel member of the neuropilin family,
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SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
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PROSITE; PS50060; MAM_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; A22 (SHOWN HERE), A0 ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

SIMILARITY: CONTAINS 1 MAM DOMAIN.
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PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVE--EPSDGT 118
                                    MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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PF00629; MAM; 1.
PF00754; F5_F8_type_C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:8005; NRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit
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IPR000998;
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AAC51789.1; -.
AAC12922.1; -.
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Pred. No. 2.8e-06;
0; Mismatches 70;
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F5/8 TYPE
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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G (IN ISOFORM A17).
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CHILDON STREET OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANGGENESIS OUTSIDE THE NERVOUS CERTAIN NEURONAL CIRCUITS AND IN ORGANGGENESIS OUTSIDE THE NERVOUS CIRCUIT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT DINGTON TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-15S ISOFORM OF VEGF-10DING TO KDR AS INCREASED CHEMOTAXIS.

CIRCUIT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).

CIPCUIT SUBCELLULAR LOCATION: Type I membrane protein.

CIPCUIT SUBCELLULAR FOOUND IN THE EMBRYONIC NERVOUS SYSTEM.

CIPCUIT SIMILARITY: CONTAINS 2 CUB DOMAINS.

CIPCUIT SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QWJ9;
16-OCT-2001 ()
16-OCT-2001 ()
16-OCT-2001 ()
Neuropilin-1 ()
                         PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1;
PROSITE; PS01286; FA58C_2;
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                               Pfam;
 Transmembrane; SIGNAL
                                                                                            PRINTS; PR00020; MAMDOMAIN. SMART; SM00042; CUB; 2. SMART; SM00231; FA58C; 2. SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                 EMBL; AF016296;
HSSP; P12259; 10
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                    Pfam; PF00754; F5_F8_type_C;
                                                                                                                                                                 Pfam; PF00629; MAM;
                                                                                                                                                                                                                                                                                         or send an email
                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 90:753-762(1997)
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MEDLINE=97433085; PubMed=9288754;
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                                                                                                                                                                                                                        InterPro;
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Eukaryota; Metazoa; Chordata;
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IPR000998;
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Glycoprotein;
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                                                                                                                                                                                                                    CUB_domain.
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            Neurone; Signal;
  POTENTIAL
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            Receptor.
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CHAIN DOMAIN

POTENTIAL.
CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

NEUROPILIN-1.

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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16-OCT-2001 (Rel., 40, Created)
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                                                                                                                                                                                                                                                                                             "Neuropilin is a semaphorin III receptor."; Cell 90:753-762(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor
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                                                                        This
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           SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content is
                                                                                                                                                                              FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM SUBCELLULAR LOCATION: Type I mortdein.

TISSUE SPECIFICITY: FOUND IN CERTARIN NEURONAL POPULATIONS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCILLINING IN THE RIBS.
                                                                                                       SIMILARITY: BELONGS TO THE NEUROPILIN SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOM SIMILARITY: CONTAINS 1 MAM DOMAIN.
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vengood D.V., Rowe
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r (Vascular endothelial cell
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Sciurognathi; Muridae
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Usage
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and for
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RESULT 9
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Best Local S
Matches 45
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Pfam; PF00754; F5_F8_type_C; 2
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01286; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS01286; FA58C_2; 2.
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                                                      VEGD_RAT STANDARD; PRT; 326 AA. 035251; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Vascular endothelial growth factor D precursor growth factor) (FIGF).
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CARBOHYD
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DOMAIN
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                           Rattus norvegicus (Rat).
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HSSP; P12259; 10
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IPR000998;
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Rodentia;
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BY SIMILARITY.
BY GILCNAC.
N-LINKED (GLCNAC.
MELINKED 
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Pred.
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              Craniata; Vertebrata;
Sciurognathi; Muridae;
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No. 3.
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                           Euteleostomi;
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Ra Submitted (JUI-1997) to the EMBL/GenBan/GenBasses.

Control (JUI-1997) to the EMBL/GenBan/Genesis, lymphangiogenesis of the in angiogenesis, lymphangiogenesis of the interest of the vertical control and also has effects on the permeability of blood migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and control of the vertical control of the venous and lymphatic endothelium in adults. Binds and control of the vertical control
                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                       Matches
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00249; PDGF_1; 1. PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00341; PDGF; 1 Pfam; PF03128; CXCXC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000072; PD_growth_fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF014827; AAB66557.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                      LYRPTWQLLGKAFVFGRKSR------VVDLNLLTEEVRLYSCTPRNFSVSIREE 262
LWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTETLKVIDEEWQRTQCSPRETCVEVASE
                                                                                                                   GFSIEHRAVKDVSLERSSRSVLERS-----
                                                                                                                                                                       GFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLED
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                                                                                                                                                                                                                                                                                                                                                     227
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194
141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residues; Multigene
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INTRACHAIN (BY SIMILARITY).

INTRACHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                 Score 162.5;
Pred. No. 1.1e
23; Mismatches
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INTRACHAIN (BY :
INTRACHAIN (BY :
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X(1,3)-C.
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                                                                                                                                                                                                                                                                                                                                                        1261AFA373596C00 CRC64;
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                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RT neuropilin, in the mouse nervous system.";

2. J. Neurobiol. 29:1-17(1996).

2. C. FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS CIRCUITS OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS INCREASED CHEMOTAXIS.

2. C. IT MAY REGULATE VEGF-INDICED ANGIOGENESIS (BY SIMILARITY).

3. C. IT MAY REGULATE LOCATION: Type I membrane protein.

3. C. IT SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

3. C. IT SIMILARITY: CONTAINS 2 CUB DOMAINS.

3. C. IT SIMILARITY: CONTAINS 1 MAM DOMAIN.
                           SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2
PROSITE; PS01286; FA58C_2; 2
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS00060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRP1_MOUSE
P97333;
01-NOV-1997
                                                                                                                                                       Pfam; PF00629; MAM; 1.
Pfam; PF00754; F5_F8_type_C;
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend-an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, L
16-OCT-2001 (Rel. 40, L
Neuropilin-1 precursor
NRP1 OR NRP.
                                                                                                                                                                                                        InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawakami A., Kitsukawa T., Takagi S., Fujisawa I Developmentally regulated expression of a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
 SIGNAL
                                                                                                                                                                                           Pfam; PF00431; CUB;
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c: TISSUE=Embryonic brain; MEDLINE=96353149; PubMed=8748368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      MGD; MGI:106206; Nrp
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P12259; 1CZT.
Glycoprotein;
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35, Last sequence update)
40, Last annotation update)
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Rodentia;
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                Neurone; Signal;
   POTENTIAL.
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                   Repeat; Receptor.
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NRP2_MOUSE
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Best Local Similarity 36.5
Matches 42; Conservative
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLOFT-2 ISOFORM OF PGF
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLOFT-2 ISOFORM OF PGF
-: SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
-: SUBCELLULAR LOCATION: Type I membrane protein
-: ALTERNATIVE PRODUCTS: 6 ISOFORMS; AS (SHOWN HERE), AO, A5, A17,
BO AND B5, ARE PRODUCED BY ALTERNATIVE SPLICING.
-: TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME
NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,
INTESTINAL ERTHHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
-: SIMILARITY: BELONGS TO THE EXPRESSION PATTERN IS VERY DYNAMIC AND
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
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                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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MEDLINE-97470888;
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                                                                                                                                                                                             affinity receptor for the semaphorins
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE
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EXTRACELLULAR (POTENTIAL).
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CRC64;
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Pfam; PF00431; CUB; 2.
Pfam; PF000529; MAM; 1.
Pfam; PF000754; F5_F8_Type_C; 2
SMART; SM00042; CUB; 2.
SMART; SM00031; FA58C; 2.
SMART; SM000317; MAM; 1.
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EMBL; AF022854; AAC53377.1; -
EMBL; AF022855; AAC53378.1; -
EMBL; AF022857; AAC53380.1; -
EMBL; AF022861; AAC53382.1; -
EMBL; AF022861; AAC53382.1; -
HSSP; P12259; 1CZT.
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SEQUENCE
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PROSITE; PS01285; FA58C_1;
PROSITE; PS01286; FA58C_2;
PROSITE; PS50060; MAM_2; 1
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POLY-SER.
BY SIMILARITY.
BY SI
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CUB 1.
CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                      > GTLPPGTEPTVDTVPVQPIPAYWYYMAAGGAVLVLAS
VVLALVLHYHRERYAAKKTDHSITYKTSHYTNGAPLAVEPT
LTIKLEQERGSHO (IN ISOPORM B0).
VDIPETHGGEGYEDEIDDEYEGDWSNSSSTSGAGDPSSGK
EKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCTCSYS
GLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA -> G
GTLPPGTEPTVDTVPVQDIPAKWYYVMAAGGAVLCLASVL
ALVLHYHRERYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
Score 160.5;
                                                                                                              KLEQERGSHC (IN ISOFORM B5).
G -> I (IN REF. 1; AAC53380/AAC53381).
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DΒ
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A0).
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TLD_BRARE
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                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
EMBL: AF027596; AAC60304.1; -. HSSP; P3555; 1EMN.
MEROPS; M12.016; -. ZFIN; ZDB-GENE-990415-265; tolloid.
InterPro; IPR001506; Astacin.
InterPro; IPR000152; Asx_hydroxy1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98057457; PubMed=9395394;
Blader P., Rastegar S., Fischer N., Straeh
"Cleavage of the BMP-4 antagonist chordin
Science 278:1937-1940(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       Development 126:3119-3130(1999)
                                                                                                                                                                                                                                                                                                                                                                           "The role of tolloid/mini fin
                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION, AND TISSUE SPECIFICITY. MEDLINE=99307076; PubMed=10375503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mini fin protein).
TOLLOID OR TLD OR MFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dorsal-ventral patterning tolloid protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057460;
                                                                                                                                                                                                                                                                                                                                                              zebrafish embryo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                    closing blastopore with greater expression ventral animal pole, expressed in the ectoderm flanking neural plate. At the 10-somite stage, expressed tailbud and cranial neural crest. At the 20-somi expressed in the hematopoietic system. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                    FUNCTION: Required for patterning ventral tissues of increase bone morphogenetic protein (BMP) activity gastrulation by proteolytic cleavage of chordin and from inactive complexes.

TISSUE SPECIFICITY: During gastrulation, accumulate the protein active complexes.
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() Teleostei; Osta
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hordin by
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Ostariophysi; Cypriniform
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Pfam;
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   691
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  LSSDSKLHGKYCGT-EVPEVITSQYNNMRIEFKSDNTV-SKKGFKAHF
                  -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY
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IPR001881;
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PRINTS: PR00480; ASTACIN.
SMART; SM00042; CUB; 5.
SMART; SM00181; EGF; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00010; ASX_HYDROXYL;
PROSITE; PS010180; CUB; 5.
PROSITE; PS00022; EGF_1; FALSE_1
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS00142; ZINC_PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental protein;
               NGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE-
NGTITTPGWPKEYPPNKNCVWQVVAPTQ-YRISMQF-EAFELEG--NEVCKYDYVEVRSG
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                                                    Similarity 39.0
43; Conservative
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156
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EGF-like.
EGF_Ca.
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; EGF-like domain;
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N-LINKED (GICNAC...
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BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
BY SIMILARITY.
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POTENTIAL.
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                                                     Mismatches
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                                                                            Length 1022;
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RESULT
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30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                     Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino form of vascular endothelial growth factor (VEGF) and of placer growth factor-2, but only neuropilin-2 functions as a receptor the 145-amino acid form of VEGF.";
J. Blol. Chem. 275:18040-18045(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "identification of a natural soluble endothelial growth factor: In vivo ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOKET S., Takashillad S., Mido H. V., Net
"Neuropilin-1 is expressed by endotheli
isoform-specific receptor for vascular
Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gagnon M.L., Bielenberg D.R., Soker S., Klagsbrun M.; "Identification of a natural s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Prostatic adenocarcinoma; MEDLINE-20183929; PubMed-10688880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRP1_HUMAN
ISOFORM IS SECRETED.

ISOFORM; MEMBRANE-BOUND (SHOWN HERE)
ALTERNATIVE PRODUCTS: 2 ISOFORMS; MEMBRANE-BOUND (SHOWN HERE)
AND SOLUBLE/SNRP1; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND
SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE
BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT
TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY ]
NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN 1
                                                                                                                                                                                                                                                     FUNCTION: THE MEMBRANE-BOUND ISÓFORM IS A RECEPTOR INVOLVED IN DEVELOPMENT OF THE CARDJOVASCULAR SYSTEM, IN ANGIOGENESIS, IN TORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED
                                                                                                                                                                         FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOO
                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE
                                                                                                                                                           VESSEL NUMBER AND INTEGRITY.
                                                                                                                                                                                                                                           ANGIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90:739-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR NRP OR VEGF165R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tessier-Lavigne M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      060461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SOLUBLE/SNRP1 ISOFORM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., Miao H.-Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gechtman Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97:2573-2578(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOFORM), AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ufeld G., Klagsbrun ial and tumor cells endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miao H.-Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                      for the 165-amino acid VEGF) and of placenta ions as a receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell growth
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                                                                THE MEMBRANE-
                                                                                                                                           SOLUBLE/SNRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takashima
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Query Match
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00020; MAMDOMAIN. SMART; SM00042; CUB; 2. SMART; SM00231; FA58C; 2. SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                Pfam;
Pfam;
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EMBL; AF145712;
HSSP; P12259; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND PLACENTA; MODERATELY IN LUNG, LIVER, S
AND PANCREAS; AND LOW IN ADULT BRAIN. THE
PARTOCYTES, KIDNEY DISTAL
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                                                                                                                                                                                                                                                                                                                                                                                                  PF00431;
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          Similarity
                                                                                                                                                                                                                                                                                                                 PS01180; CUB; 2.
PS01285; FA58C_1;
PS01286; FA58C_2;
                                                                                                                                                                                                                                                                                                 PS00740; MAM_1; PS50060; MAM_2;
                                                                                                                                                                                                                                                                                                                                                                                                         IPR000859; CUB_domain
IPR000421; FA58_C.
IPR001092; HLH_basic.
IPR000998; MAM_domain
                                                                                                                                                                                                                                                                               splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROT entry is copyright. It is produced Swiss Institute of Bioinformatics and
                                   AA;
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                                                                                                                                                                                                                                                                                                                                                                                          MAM;
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        8.5%;
35.7%;
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                                                                    N-LINKED (GLCNAC...) (POT)
EPP -> GIK (IN SOLUBLE/SNRP)
MISSING (IN SOLUBLE/SNRP1 I:
Score 158.5;
Pred. No. 9.3e
18; Mismatches
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K -> E (
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F5/8
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                                                                                                                                   SIMILARITY. SIMILARITY.
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      DB
-06;
                                                                              SOLUBLE/SNRP1
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E SOLUBLE/
L AND PROX
                 1;
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                Length
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L outstation -
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RESULT 14

NRP1_CHICK
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                    PROSITE;
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or send a
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modified and this statement
entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developing chick nervous system.";
Dev. Biol. 170:207-222(1995).
-!- FUNCTION: RECEPTOR INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=White leghorn;
MEDLINE=95324761; Publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, I
16-OCT-2001 (Rel. 40, I
Neuropilin-1 precursor
                                                                                                            SMART; SM00231; FA58C; 2. SMART; SM00137; MAM; 1.
                                                                                           PROSITE; PS01180; CUB; 2
                                                                                                                                               SMART; SM00042; CUB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRP1 OR NRP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL BLOOD VESSELS IN THE ENTIRE EMBRYO.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTI (LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANGENRESIS OUTSIDE THE NERVOUS SYSTEM, IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY). SEEMS
                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPERTIES
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                                                                                                                                                           PF00629; MAM; 1.
PF00754; F5_F8_type_C;
S: PR00020; MAMDOMAIN.
                                                                                                                                                                                                                      PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                  an
                    PS00740; MAM_1; PS50060; MAM_2;
                                                    PS01285; FA58C_1; 2.
PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                       IPR000421;
IPR000998;
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                                                                                                                                                                                                                                                                                                                                        nd this statement is not removed. equires a license agreement (See email to license@isb-sib.ch).
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Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ynorn; TISSUE-Embryonic b
1; PubMed-7601310;
7a Y., Shimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             νευ).
Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                  institutions as long
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Last annotation update)
or (A5 protein).
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ID PCO1_HUMAN
AC Q15113; O14550;
DT 30-MAY-2000 (Rel
DT 30-MAY-2000 (Re
15-JUN-2002 (P
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Kessler E.
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                                                                                       TISSUE=Heart;
                                                                                                          SEQUENCE FROM N.A
                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCOLCE
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                    Struct.
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE)
procollagen COOH-terminal proteinase enhancer) (Type 1 proc
            Hirahara I., Syoufuda K.,
Morisaki N., Saito Y.;
"Smooth muscle cell derive
                                                                                                                                                "Type I procollagen COOH-terminal proteinase enhancer protein: identification, primary structure, and chromosomal localization cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                    Takahara K., Kessler E., Biniaminov L.,
Jani-Sait S., Shows T.B., Greenspan D.S
                                                                                                                                                                                                                              MEDLINE=95014462; PubMed=7523404;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSEIILEFESFE-----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIREVSDEYFPSEPGFCIHYNIVM--P
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                                                                                                                                                                                      procollagen COOH-terminal
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                                                                                                                                                                                                                                                                                                                                                   enhancer protein)
                                                                                              observations
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Funct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Primates;
 derived procollagen 21:662-662(1996).
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29.4%;
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                                        Harada K.,
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Pred. No. 1.2e
27; Mismatches
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F5/8 TYPE
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NEUROPILIN-1
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                        Tomita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 449
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             C-protease
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.2e-05;
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                                         Urakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 914;
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               enhancer
                                                                                                                                                                                                                  Eddy R.L.,
                                                                                                                                                                                                                                                                                                                                                                 procollagen
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  Query Match
Best Local Similarity
Matches 48; Conserv
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                                                                                                                  CARBOHYD
CARBOHYD
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00431; CUB; 2. Pfam; PF01759; NTR; 1. SMART; SM00042; CUB; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB008549; BAA23281.1;
EMBL; AF053356; AAC78800.1;
EMBL; AF083655; AAD16041.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
MEDLINE=20092917; PubMed=10625689;
MOLT J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
MEDLINE-99134301; PubMed-9933570;
Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
"Structural organization and expression patterns of the human and mouse genes for the type I procollagen COOH-terminal proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L33799; AAA61949.1; ALT_SEQ. EMBL; AB008549; BAA23281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteinase enhancer releases a metalloproteinase
J. Biol. Chem. 275:1384-1390(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsui L.-C., Rosenthal A.; "The policy of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci reveals 17 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 600270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
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[5]
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Gloeckner G., Scherer S., Schatte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Post-translational proteolytic processing of procollagen C-terminal proteinase enhancer releases a metalloproteinase inhibitor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000859; CUB_domain.
InterPro; IPR001134; Netrin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: BINDS TO THE COOH-TÉRMINAL PROPEPTIDE OF TYPE I PROCOLLAGEN AND ENHANCES PROCOLLAGEN C--PROTEINASE ACTIVITY. FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE METALLOPROTEINASE INHIBITORY ACTIVITY.

SUBCELLULAR LOCATION: Secreted.
PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 NTR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:8738; PCOLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.";
55:229-234(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                PS01180; CUB;
                                                                                           431
449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8:1060-1073(1998).
    Conservative
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                       8.3%;
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                                                                                             MW;
    22;
                                                                                                                CLEAVAGE.
N-LINKED
N-LINKED
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CLEAVAGE.
CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PROCOLLAGEN
PROTEIN.
                                                                                                                                                                                                                                                                        CUB 1.
CUB 2.
NTR.
                         Score 154; DB 1; Pred. No. 9.1e-06;
                                                                                                                                                                                                                                                   CLEAVAGE
                                                                                        -LINKED (GLCNAC. . .) (POTENTIAL)
-LINKED (GLCNAC. . .) (POTENTIAL)
3D88430158648796 CRC64;
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                 C-PROTEINASE ENHANCER
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    50;
                                              Length 449;
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Gaps
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                                                                                                        GTLTTPNWPESDYPPGISCSWHIIAPPDQV-IALTF-EKFDLE--PDTYCRYDSVSVFNG
                                                                                                                                   GSIHSPRFPHT-YPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEV---
GQGPGPKRGTEPKVKLPPKSQP
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                         -EAVSPSV-LPPSALP
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Search completed: April 29, 2003, 09:06:11 Job time: 14 secs

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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZV
FILE REFERENCE: 98-60
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US-09-457-066-43
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Best Local Similarity
Matches 345; Conserv
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LENGTH: 345
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CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                           LENGTH: 34
TYPE: PRT
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VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
                                            LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                        LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
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US-08-936-135-14
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US-09-936-135-16
US-08-915-795-8
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US-08-915-795-8
US-08-839-008-7
US-09-032-523-9
US-09-932-523-9
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Pred. No. 5.3e-195;
Mismatches 0;
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Match

Query

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Maximum

Post-processing:

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Sequence Title: Perfect score:

protein 9

Scoring table:

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VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG

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GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID MOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID MO 2
LENGTH: 345
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Best Local Similarity
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LENGTH: 345
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APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHG
TITLE OF INVENTION: PROTEIN I AND NUCLEIC ACIDS ENCODING SAME, TH
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REFERENCE: P1122
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ORGANISM: Human
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Pred. No. 4.6e-175;
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; TYPE: PRT
; ORGANISM: Human
US-09-265-686-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 345
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Best Local Similarity
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Best Local Similarity
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PRIOR ETLING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR ETLING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/265,686 CURRENT FILING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POL
FILE REFERENCE: P1122P2
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181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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                                                            GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
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87.0%;
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87.0%; Pred. No. 4.6e-175;
tive 27; Mismatches 18;
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Pred. No. 4.6e-175;
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LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL

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APPLICANT: Gilbertson, Debra G.

APPLICANT: Hart, Charles E.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF

TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVE

FILE REFERENCE: 00-28

CURRENT APPLICATION NUMBER: US/09/540,224

CURRENT FILLING DATE: 2000-03-31

EARLIER APPLICATION NUMBER: US 60/180,169

EARLIER FILLING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

US-09-540-224-5
                        Sequence 37, Application US/09457066
Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
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Best Local Similarity
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APPLICANT:
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Shoemaker, Kimberly E. Gilbertson, Debra G.
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87.0%; Pred. No. 4.6e-175;
27: Mismatches 18;
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SOFTWARE: FastSEQ for Wir
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09540224 Patent No. 6468543
                                                                                       Query Match
Best Local 9
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                                                                        Matches
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CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
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TYPE: PRT
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                                                                                       40.7%; Score 752; DB 4; Length 370; 45.3%; Pred. No. 3.3e-74;
                                                                     59;
                                                                        Mismatches
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEO ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
09-540-224-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 LEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLLKEEVKLYSCTPRNF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                            318 CSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                  236 VNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ
                                                                                                                                                                                                                                                                                    176 LPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKV 235
                                                                                                                                                                                                                                                                                                                                                   134 TSKGNHIRIRFVSDEYFPSEPGFCIHYSII---MPQVTETT------SPSV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 IKRRGRAKTMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 SYSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 VEDILKYFNPESWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
                                                                                                                    296 CVPRKVTKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                             201 TDP-TLTADALDKTVAEFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK-
                                                                                                                                                                                                                                                                                                                                                                                                         82 WLRS-QEKTRIQLSEDHQFGLEEAENDICRYDEVEVEEVSESSTVVRGRWCGHKEIPPRI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 RLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 QRASIKALRNAN----LRRDESNHLTDLYQREENIQVTSNGHYQSPRFPNSYPRNLLLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 QRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVW 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 151; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSRTNQIKITFKSDDYFVAKPGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPSI
                                                                                                                                                               VDLDRLNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.4%; Score 746.5; DB 4; 43.5%; Pred. No. 1.3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 370;
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RESULT 10
US-08-872-757-2
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08872757 Patent No. 6258584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.8%;
Best Local Similarity 42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08572225 Patent No. 5807981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 13-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,22
                                                          APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Aleksander
TITLE OF INVENTION: PROCESSES; METHODS AND USES:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-854-360
                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 456
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CITY: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE: Pennle & Dumberleas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                              Prockop, Danger Prockop, Dange
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                                                                                                                                                                                                                                                                                   Hojima, Yos
Li, Shi-Wu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prockop,
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                                                                                                                                                                                                                                                                                                                                                 Darwin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
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Pred. No. 8.8e-11;
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TREATMENT OF
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

10036-2711

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                                                  SOFTWARE: Pa
SEQ ID NO 6
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09374135 Patent No. 6277972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
ORGANISM: Mouse
-09-374-135-6
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                          TITLE OF INVENTION: BPC-1: A SECULE TITLE OF INVENTION: SECRETED BY PROSTATE 1715 OF PREFERENCE: 1703-017.US1
                                                                                                                      PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 1998-08-10
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/374,135
                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-854-3660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   706 PALQPP 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 LTAHSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF-----FSENR 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 PSVLPP 178
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SOFTWARE: Paten+T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 10-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/609,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                       PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halluin, Albert
                                                                                                                                                                                                                                                                                                   Afar, Daniel E.
Hubert, Rene S.
Leong, Kahan
                                                                                                                                                                                                                                                                Raitano, Arthur B.
Saffran, Douglas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415-854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/872,757
10-JUN-1997
                                                                                                                                                                                                              \mathtt{BPC-1}\colon A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED SECRETED BY PROSTATE AND BLADDER CANCER CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.6%;
                                                                                                                                         60/095,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8389-028-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 177.5; DB 4:
Pred. No. 1.9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 15; Gaps
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                  Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ginty, David
TITLE OF INVENTION: SEMAPHORIN RECEPTOR
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-JUL-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                   120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM -- PQVTET-TSPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155
                                                                                                NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE-- 113
                                                                         43 GYPHSYHPSEKCEWLIQAPEPYQRIMINFNPHFDLEDRD---CKYDYVEVIDGENEGGRL 99
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/052,762 FILING DATE: 17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 17-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 101
                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
                                                                                                                                                  7 LLCATLALALAG------AFRSDKCGG----TIKIENPGYLTSP 42
                                                                                                                                                                                       2 LLLGLLLTSALAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSGL 56
                                                                                                                                                                                                                               56;
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 175; DB 4; 42.1%; Pred. No. 1.5e-11;
                                                                                                                                                                                                                         9.3%; Score 172; DB 4; 131.5%; pred. No. 1.1e-09; 31.5%; mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/116,473
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                                                                                                                                                                                                                                                              Length 922;
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RESULT 13 US-08-936-135-6

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US-08-872-757-4
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                                                                                                                                    Patent No. 6258584
                                                                                                                                                      Sequence 4, Application US/08872757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6054293 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6,
                                                                                                  GENERAL INFORMATION:
APPLICANT: Procko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,0
REFERENCE/DOCKET NUMBER:
              APPLICANT: Sieron, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
                                                                                                                                                                                                                                           100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSONYTAPT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             43 GYPHSYHPSEKCEWLIQAPEPYQRIIINFNPHFDLEDRD---CKYDYVEVIDGENEGGRL 99
                                                                                                                                                                                                                                                                                                                                                62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                2 LLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                                                                                                                                                                                                                LLCATLALALAG------AFRSDKCGG----TIKIENPGYLTSP 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        923 amino acids
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                                                                                Hojima,
                                                                                                  Prockop, Darwin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                    Li, Shi-Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tessier-Lavigne, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
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                                Aleksander
RECOMBINANT C-PROTEINASE AND
                                                                                  Yoshio
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                PROCESSES; METHODS AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 169; DB 3; 1
Pred. No. 2.4e-09;
1; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 923;
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                                                                                                                                                                                                                                                                                                                                 Sequence 3, Approx No. 5939321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 01-MAR-1996
               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     TITLE OF INVENTION: Mammalian Tolloid-Like Protein NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                   APPLICANT:
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                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palant
                                                                                                                                                                                                                                                                                                                                                                                                                                       655 LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700
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                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415 CT TELEPHONE: 415-854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 10-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
APPLICATION NUMBER:
                                                                                                                    ZIP: 53703
                                                                                                                                  COUNTRY:
                                                                                                                                                     STATE:
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1155 Avenue of the Americas
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                               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                   Greenspan, Daniel S
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 3.4e-09;
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER:
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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AAY30023 AAB48657	AAY33679 AAY41766	AAE13213	AAE00998	AAY84559	AAY96861	AAB48658	ID
Human vascular end Human zvegf3, SEQ	Human VEGF-E prote Human PRO200 prote	Mouse Platelet-der	Mouse Zvegf3 prote	A murine platelet-	Murine vascular en	Mouse zvegf3, SEQ	Description

45	44	43	42	41	40	39	38	37	36	ა 5	. 34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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ALIGNMENTS

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RESULT 1
AAB48658
             Mus musculus
                                                                    09-MAR-2001
                                                                              AAB48658;
                                                                                        AAB48658 standard; Protein; 345
                                                          Mouse zvegf3, SEQ ID NO:35.
                                                                    (first entry)
                                                                                        AΑ
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03-MAY-1999; 10-NOV-1999; 04-FEB-2000; 20 Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; murine; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia; immunomodulation; hepatic. Gilbert T, WO200066736-A1. 03-MAY-2000; 2000WO-US40047 09-NOV-2000. (ZYMO) ZYMOGENETICS INC. Hart CE, 99US-0304216. 99US-0164463. 2000US-0180169. Sheppard PO, Gilbertson DG;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids; the recombinant expression of human zvegf4; an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a cell-surface polypeptides; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells treatment of ischaemia, in wound healing, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAB48654) characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 fusions; expression constructs and host cells comprising human zvegf4 nucleic acids; the recombinant expression of human zvegf4; an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 130-131; 143pp; English.
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                                                                                                                                                                                         LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                                                                              LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                              PKFPHTYPRNMYLVMRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                             VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
                                                                                                         VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                    LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Pred. No. 6.4e-182;
; Mismatches 0;
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ΧX AAY96861

AAY96861 standard;

Protein;

345

ΑA

Qy

1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS

Matches

345;

Conservative

0,

0;

Indels Length

Gaps 60

0;

345; 0;

Local

Similarity

100.0%;

Score 1848; DB 21; Pred. No. 6.4e-182; Mismatches

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C(PDEF) family. The CUB domain shows homology to CUB domains in C neuropilins, human bone morphogenetic protein. L porcine seminal plasma C protein, bovine acidic seminal fluid protein and Xenopus laevis CC tolloid-like protein. Structural analysis and homology predict that CC ZVEGF3 polypeptides complex with a second polypeptide to form multimeric C proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3. CC proteins suseful for stimulating the growth of fibroblasts or smooth CC muscles cells, for activating cell surface PDGF-alpha receptor and for C inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3 CC diabetic retinopathy, ischemic limb disease, peripheral vascular CC disease, myocardial ischemia, vascular intimal hyperplasia, and continuous c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1998;
06-JUL-1999;
21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This shows a murine ZVEGF3 a novel vascular endothelial growth factor homologue. Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel zvegf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising epitope bearing portion of a specific amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 169-170;
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99US-0142576.
99US-0161653.
99US-0165255.
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03-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
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The present sequence represents murine platelet-derived growth factor (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor.
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12-NOV-1998;
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ELSINKI LICENSING
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                                                                                                                                                                                                                                                   Mouse; Zvegf3 antagonist; cell proliferation; stellate cell activation; extracellular matrix production; fibrosis; VEGF-R; PDGF-C; platelet-derived growth factor; PDGF; vascular endothelial growth factor; VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder; chronic active hepatitis; fulminant viral hepatitis; amyloidosis; diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis; assestosis; renal arteriosclerosis; post necrotic cirrhosis;
                                                                                                                                                  diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis; pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis; bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
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Pred. No. 6.4e-182;
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12-NOV-1999;
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               VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
                                                                                                                                                                                                                                                                                                                                                         MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                   LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                    GRWCGSGTVPGKQTSKGNHIRIREVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                                                      GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
                                                                 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK . 300
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                                                                                                                                                  LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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Pred. No. 6.4e-182;
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Similarity

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RESULT 5
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12-NOV-1999;
31-MAR-2000;
07-DEC-1999;
                                                                                             The sequences given in AAB47889-90 represent human and mouse zvegf3, respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog and it was used in the method of the invention for promoting growth of bone, ligament or cartilage and stimulating proliferation of osteoblasts or chondrocytes in a mammal. The proteins used were preferably a dimeric protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3 protein, with a delivery vehicle. The method of thinvention is useful for promoting growth of bone, ligament or cartilage in a mammal, where the composition is administered at a site of a bony defect, preferably a fracture, bone graft site, implant site, or periodontal pocket, and mammal. It is further useful for promoting proliferation of osteoblasts, osteoclasts, chondrocytes or bone marrow stem cells are harvested from a patient prior to culture. The
                                                                                                                                                                                                                                                                                                                                           Promoting growth of bone, ligament or cartilage in a mammal, administering to the mammal a protein which comprises growth domain of zvegf3 protein, a homolog of platelet-derived growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implant; periodontal
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                                                          Sequence
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GILBERTSON D
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                                                                                   therefore useful for treating osteoporosis.
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Matches 345; Conserv
                                                                                                                                                             The patent discloses a method for producing a transgenic, non-human animal over-expressing a platelet derived growth factor C (PDCF-C), or its functional fragment or analogue. The method involves introducing a transgenic PDGF-C DNA into a cell of a non-human animal, introducing the cell into a non-human animal and allowing the cell to develop into a transgenic, non-human animal. The transgenic animal is useful as a model to study disease states characterised by over-expression of PDGF-C and to find therapy for those diseases, particularly hypertrophy and fibrosis in various organs including the heart. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             A transgenic animal over-expressing platelet derived growth factor C useful to study and find therapy for disease associated with PDGF-C over-expression, including cardiac hypertrophy and fibrosis -
                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 42-43;
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                                                                                                                                               PDGF-C
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RESULT 7
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В
       This invention describes the isolation of a novel human vascular endothelial cell growth factor E (VECF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VEGF-E can be administed therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy It can be combined with a carrier in pharmaceutical compositions, which is the combined with a carrier in pharmaceutical compositions, which is the combined with a carrier in pharmaceutical compositions, which is the combined with a carrier in pharmaceutical compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue generation; regeneration; angiogenic disorder; age-related neovascularization; tumor; gene r
                                                                                                                                                                   endothelial
                                                                                                                                                                                New
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02-NOV-1998;
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                                                                                                                                       Claim 1;
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DB; AAZ23691.
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                                                                                                                                                               factor polypeptide useful disorders, e.g. cardiac l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           man; vascular endothelial cell growth factor; wound repair;
cardiovascular disorder; endothelial disorder; therapy;
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98US-0184216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             egeneration; cardiac hypertrophy; cancer; detection;
age-related macular degeneration; vascular disease;
                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the mathod of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies,
                                                                                                             Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
                                                                                                                                                             Human
                                                                                                                                                                                   07-DEC-1999
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 10-MAR-1998;
                      08-MAR-1999;
                                                                     W09946281-A2
                                                                                                                                                                                                                                 AAY41766 standard; Protein; 345 AA.
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                                              16-SEP-1999
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                                                                                                                                                             protein sequence.
                       99WO-US05028.
98US-0077450
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87.0%;
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Pred. No. 3.2e
27; Mismatches
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8.2e-163;
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21-APR-1998;
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09-APR-1998;
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31-MAR-1998;
31-MAR-1998;
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01-APR-1998;
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9805-0080334
9805-0081049.
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9805-0081105.
9805-0081203.
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9805-0081817.
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9805-0081952.
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30-JUL-1998
30-JUL-1998
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                                                                                                                                                                                                                                                                                                                                       and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                             MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                  1999-551358/46
DB; AAZ34296.
          VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
                                                    LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                          LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                                                                                                                                                                                                    MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating blood on disorders -
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A,
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                                                                                                                                                                                                                                                                 Conservative
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98US-0086032.
98US-0086414.
98US-0086486.
98US-0086486.
98US-0087098.
98US-0087208.
98US-0087208.
98US-004651.
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                                                                                                                                                                                                                                                                          90.2%;
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                                                                                                                                                                                                                                                                          Score 1667;
Pred. No. 3.
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1.2e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP,
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RESULT 9 AAY30023

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Best Local :
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27-JAN-1998;
05-JUN-1998;
24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a vascular endothelial growth factor related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that antagonize its activity. VEGF-R antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting tumour growth and for treating cancer. VEGF-R itself can be used to stimulate tissue growth, angiogenesis and to treat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of the VEGF-R protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 56-58; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A vascular endothelial growth factor related protein and related polynucleotide, useful for identifying antagonists and binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dou
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                                                                                                                                                                                                                                                                                  MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
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                                      LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                   LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                                                                                                                                                               LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKEPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
                                                                                                                                             LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERITTVSTNGSIHS
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98US-0072635.
98US-0088089.
98US-0090544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1667;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
8.2e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
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                       The invention relates to the human growth factor homologue zvegf4 CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member CC of the PDGF (platelet-derived growth factor)/YEGF (vascular endothelial CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654) CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like CC characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like CC activity, having mitogenic activity on fibroblasts, vascular smooth CC growth. The invention also relates to fusion proteins comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or growth. The invention also relates to fusion proteins comprising human zvegf4 nucleic acids; the recombinant expression of human zvegf4/human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a cell-surface polypeptides; and a method of detecting a genetic cell-surface polypeptides; and a method of detecting a genetic cell-surface polypeptides; and a method of detecting a genetic cell-surface polypeptides; and a method of detecting a genetic cell-surface polypeptides; and a method of detecting a genetic cell-surface polypeptides; and a method of detecting a genetic cell-surface polypeptides; and a method 
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10-NOV-1999;
04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB48657 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-2000
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DB; AAC81582.
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99US-0164463.
2000US-0180169.
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RESULT 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation
                                                          Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and
                                                                                                                                                                                                                                                                                                atherosclerosis; PDGF-related protein; antiarteriosclerotic
                                                                                                                                                                                                                                                                                                                                               Human platelet-derived growth factor related protein
                                                                                              N-PSDB;
                                                                                                         WPI; 2000-664991/64
                                                                                                                                 Hammond
                                                                                                                                                       (ELIL ) LILLY & CO
                                                                                                                                                                               06-APR-1999;
                                                                                                                                                                                                    24-MAR-2000; 2000WO-US06427
                                                                                                                                                                                                                             12-OCT-2000
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                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAB24250 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune system. The
                                              treating atherosclerosis by
                                                                                                                                                                                                                                                                                                               vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                              AAC64426
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                                                                                                                                                                                                                                                                                                               endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AA;
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                                                                                                                                 Na
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                               99US-0127913
                                                                                                                                                                                                                                                                                                                         derived growth factor
                                                                                                                                                         ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        emia, in wound healing, and in the modulation of the present sequence represents human zvegf3.
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                                                                                                                                                                                                                                                                                                               growth
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                                               administering
                                                                                                                                                                                                                                                                                                               factor h;
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Pred. No. 3.2e
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        345
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                                                                                                                                                                                                                                                                                                               tissue regeneration;
                                                                                                                                                                                                                                                                                                                        related protein;
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3.2e-163;
                                               LP8
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                                              antagonist
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                                                                                                                                                                                                                                                                                                              vulnerary;
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The present invention describes a method

for

enhancing tissue

growth

Claim 4; Page 63-64;

64pp; English

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RESULT 12
AAB44322
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Matches 300
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112 - MAR - 1999
29 - MAR - 1999
21 - APR - 1999
24 - APR - 1999
14 - MAY - 1999
23 - JUN - 1999
26 - JUL - 1999
29 - OCT - 1999
30 - NOV - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LPB or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smootl muscle growth. Antagonists of LPB are useful for treating atherosclerosis. The present sequence represents human LPB, which is
                                                                                                                                                                                          WO200053756-A2
                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                             Human PRO200
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                                                                                                                                                                                                                                                                                                                                                  AAB44322 standard;
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2-MAR-1999;
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                                                                                                                                                                                                                                         sequence
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                                                                                                                                                                                                                                                                           (UNQ174) protein
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                           2000WO-US04341
        99US-0130232.
99US-0131445.
99US-0134287.
99US-0141037.
99US-0145698.
99US-0162506.
99WO-US28313.
                                                                                           99WO-US05028.
99US-0123957.
99US-0126773.
                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                       tag; detection;
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                                                                                                                                                                                                                                                    transmembrane protein;
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Pred. No. 3.2e-163;
                                                                                                                                                                                                                                                                           sequence
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                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                            SEQ ID NO:488
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                                                                                                                                                                                                                                                    EST;
                                                                                                                                                                                                                                                    cytostatic;
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AC XX

AAB10633

Protein;

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RESULT 13
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16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara N,
Goddard A,
Kljavin IJ,
Shelton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                          PKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
                                                                                                                                                                                                                                                                                                                                                MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                              LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                                     {\tt GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA}
                                                                                                                                                                                                                                                                                                                                 MSLFGLLLTSALAGOROGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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                                                                                                                                                                                                                                                                           PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL
                                                                                                                                                                                                                                                                                                                                                                                         300;
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Filvaroff E,
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AA;
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99WO-US30095.
99WO-US31243.
99WO-US31274.
2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
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                                                                                                                                                                                                                                                                                                                                                                                                   90.2%;
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Fong S, Gao W, Gerber H,
Grimaldi CJ, Gurney AL, I
der MA, Pan J, Paoni NF,
Tumas D, Williams PM, Woo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 1667; DB 21; Pred. No. 3.2e-163;
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                                                                                                                                                                                                                                                                                                                                                                                       18;
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Query Match
Best Local :
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                    121
                                                                                                                                                                                                                                                                                                                                  Local
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                            GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                             PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
                                                                                                                                                                                                                                                      MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
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GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                                                                                                      PREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL
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)B; AAA71951.
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                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                           Mismatches
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1.2e-163;
nes 18;
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vessels, growth and development of tissues, tissue regeneration and orgal and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein

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from clones 4 and 7 described in the method of

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                                                                                                                                                                                                    This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, anticheumatic antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood contributions of the province of the inventor of the province of the inventor of the province of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF-X; vascular endothelial growth factor; human; vulnerary; cytosta antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; angiogenesis regulator; vascularization regulator; cancer; coran paga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds - \frac{1}{2}
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18-MAR-1999;
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DB; AAA71955.
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iabetic; treatment;
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18-MAR-1999;
08-NOV-1999;
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Disclosure; Fig 30B; 127pp; English.
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                                                                        WPI; 2000-442669/38.
N-PSDB; AAA71990.
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                                                                                                                                                                                                                                                                                                                                                                                                            Human VEGF-X protein #4.
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                                     New vascular endothelial growth factor protein, useful for treating preventing diseases associated with inappropriate angiogenesis activ
                                                                                                           Dhanaraj SN,
                                                                                                                                                                                                                         21-DEC-1999;
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99US-0164131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote with moral treating the products of the invention are useful contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity or vascularization. This sequence represents a human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                     LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
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VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                      VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                          LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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Pred. No. 3
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Search completed: April 29, 2003, 09:05:44
Job time: 34.5 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     April 29, 2003, 09:08:16; Search time 26.5 Seconds (without alignments) 1043.199 Million cell updates/sec
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                                                                                                                                         /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	DB	ID	Description
ш	1848	100.0	345	ٔ و	US-09-852-209A-7	Sequence 7, Appli
2	1848	100.0	345	9	US-10-139-583-43	43,
ω	1848	100.0	345	10	US-09-823-033-4	4
4	1848	100.0	345	10	US-09-818-943-2	2
ហ	1667	90.2	345	9	US-09-978-295A-488	88
o	1667	90.2	345	ø	US-09-978-697-488	
7	1667	90.2	345	9	US-09-978-192A-488	
8	1667	90.2	345	9	US-10-139-583-2	Sequence 2, Appli
9	1667	90.2	345	9	US-09-999-832A-488	Sequence 488, App
10	1667	90.2	345	9	US-09-978-189-488	Sequence 488, App
11	1667	90.2	345	9	US-10-028-072-286	286
12	1667	90.2	345	9	US-10-121-049-286	Sequence 286, App
13	1667	90.2	345	9	US-10-123-904-286	286
14	1667	90.2	345	9	US-10-140-470-286	
15	1667	90.2	345	ဖ	US-09-796-753-6	6
16	1667	90.2	345	و	US-10-175-746-286	286
17	1667	90.2	345	9	US-10-176-918-286	
18	1667	90.2	345	9	US-10-176-921-286	Sequence 286, App
19	1667	90.2	345	9	US-10-103-197-4	

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
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AT TOWNSHIP	US-10-123-236	US-10-123-108	US-10-013	US-09-978	US-10-143	US-09-918-585	US-10-167	Sn	US-10-12	US-09-99	0S-09-98		US-10-14	US-10-12	US-10-01	US-09-97	US-09-97	US-09-978-403A-48	us-09-978	US-10-142	US-09-978-608	US-10-140-002	US-10-143-114	US-10-	US-10-140-474	US-10-137-865	
		286,	488,			488,	488,	286,	286,	488,	488,	488,	e 286,	286,	488,	488,	488,	488,		286,	488,	286,	•	Sequence 286, App	286,	•	

ALIGNMENTS

RESULT 1 US-09-852-209A-7

Sequence

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US-09-852-209A-7
                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 345
TYPE: PRT
                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ALITALO, KARI
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR OF TITLE OF INVENTION: THEREFOR, AND USES THEREOF FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/144,022
                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
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                                                                                                                ORGANISM: Murinae gen. sp.
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UUTELA, Marko
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Score 1848; DB 9;
Pred. No. 1.5e-155;
D; Mismatches 0;
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APPLICANT: Hart; Charles
APPLICANT: Piddington, C
APPLICANT: Sheppard, Pan
APPLICANT: Shepmarker, Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 43
LENGTH: 345
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 345; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR FILING DATE: 1999-12-07
NUMBER CONTROL DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shoemaker, Kimberly E. APPLICANT: Gilbertson, Debra G. APPLICANT: West, James W. TITLE OF INVENTION: GROWTH FACTOR HOMOLOG FILE REFERENCE: 98-60
       241
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                                                                                                                                                                                                                                                                                              MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                       LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 240
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                                                                                                                                       GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
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CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARR: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 345
TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                    APPLICANT: ERIKSSON, Ulf
APPLICANT: LI, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: AASE, Karin
APPLICANT: LI, Hong
                                                                                                                                                                                                      Sequence 2, Application US/09818943 Patent No. US20020049987A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 345; Conserv
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APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS TITLE OF INVENTION: (PDGF-C) AND USES THEREOF FILE REFERENCE: 1064/48487

CURRENT APPLICATION NUMBER: US/09/818,943

CURRENT FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/192,507

PRIOR FILING DATE: 2000-03-28
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SEQ ID NOS:

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; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae
US-09-818-943-2
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APPLICANT:
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                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C11
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APPLICATION NUMBER: US/09/978,295A FILING DATE: 2001-10-15
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Baker Kevin P.
Botstein, David
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Gao, Wei-Qiang
                                                               Williams, P. Mickey Wood, William I.
                                                                                                    Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                          Tumas, Daniel
                                                                                                                                                                                                               Gurney, Austin L.
Hillan, Kenneth J
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Grimaldi, J. Christopher
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Pred. No. 1.5e-155;
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PRIOR APPLICATION NUMBER: 60/065311
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       OR FILING DATE: 1998-04-08
RAPPLICATION NUMBER: 60/081049
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OR APPLICATION NUMBER: 60/081071
OR FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/081070
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Napier,
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                                                       Godowski, Paul J.
Grimaldi, J. Christopher
                                 Gurney, Austin L.
Hillan, Kenneth J
                                                                               Goddard, Audrey
                                                                                            Gerritsen, Mary E.
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                        Kljavin, Ivar
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                                        Sequence 488, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Botstein, David
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APPLICATION NUMBER: 60/077641
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Stewart, Timothy A.
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Hillan, Kenneth
Kljavin, Ivar J.
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Grimaldi, J. Christopher
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                                                                                                       MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
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VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
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Pred. No. 1
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345
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60/081195

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60/083392

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60/083336 60/082796

FILING DATE: APPLICATION NUMBER:

1998-04-23

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APPLICATION NUMBER: 60/083322

APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22

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60/082569 60/082568

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                                                                                                                                                                                Publication No.
                                                                                                                                                                                                Sequence 488,
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Best Local :
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LENGTH: 345
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CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
                                                                                                                                    APPLICANT: Ashkenazi, APPLICANT: Baker Kev
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Piddington, Christopher S
Sheppard, Paul O.
Shoemaker, Kimberly E.
Gilbertson, Debra G.
West, James W.
Gerritsen, Mary
              Gerber, Hanspeter
                          Fong, Sherman
Gao, Wei-Qiang
                                                          Filvaroff, Ellen
                                                                                                     Desnoyers, Luc
                                                                                                                      Botstein, 'David
                                                                                                                                  Baker Kevin P.
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/999,832A CURRENT FILING DATE: 2001-10-24
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                                                                        APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
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FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077791
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                APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/079728
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APPLICATION
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Wood, William I.
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Stewart, Timothy A.
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Grimaldi, J. Christopher
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Kuo, Sophia S.
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FILING DATE: 1998-05-07
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LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                                                           GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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                                                     LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
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APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-22

APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082568

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APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/081819 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817

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CURRENT FILING DATE: 2001-10-15
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C7
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Stewart, Timothy A.
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Hillan, Kenneth J
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ton, David L.
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Sherwood, Steven
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEO ID NOS: 550
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APPLICANT: Beresini, Ma
APPLICANT: DeForge, Lau
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                                                                     PKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
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Filvaroff, Ellen
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87.0%; Pred. No. 1
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US-10-123-904-286
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C54
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LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
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                                                 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
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o. US20030022328A1
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LENGTH: 345
TYPE: PRT
ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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 Application US/09796753 No. US20030027998A1
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Gerritsen, Mary E.
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APPLICANT: McCarth
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PRIOR FILING DATE: 2000-09-30
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                                                                                                                                               LENGTH: 345
TYPE: PRT
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R FILING DATE: 2000-03
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FILING DATE: 1999-06-18
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MILLGLILLTSALAGQRTGTRAESNISSKIQISSDKEQNGVQDPRHERVVTISGNGSIHS 60
                                                                                                                                                                                          SEQ
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Pred. No. 1.6e
27; Mismatches
                                                          .6e-139;
les 18;
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                                                                                    Length 345;
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Search completed: April 29, 2003, 09:16:57 Job time: 28.5 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   1848
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1: sp_archea:*
2: sp_bacteria
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Match
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Gapop 10.0 , Gapext 0.5
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1848
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                 Q9qy71 mus musculu
Q9qy81 mus musculu
Q9qx6 rattus norv
Q9u122 homo sapien
Q9nra1 homo sapien
Q91946 gallus gall
Q9qqt1 rattus norv
Q9gzp0 homo sapien
Q9bwv5 homo sapien
092517 mus musculu
Q9d118 mus musculu
Q8dfx6 brachydanio
057658 gallus gall
Q9jm4 mus musculu
Q91925 xenopus lae
057381 xenopus lae
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Q9jjs9 rattus norv	Q9JJS9	11	701	8.1	149	ū
	009020	11	212	8.1	149	4
2 cypr	Q9DGC2	13	686	8.1	150.5	3
2	Q9H2D4	4	906	8.4	155.5	2
homo	Q9H2E3	4	906	8.4	155.5	Ξ
homo	Q9H2D5	4	901	8.4	155.5	Ö
homo	Q9H2E4	4	901	8.4	155.5	39
homo	Q9H2E2	4	555	8.4	155.5	8
homo	Q9UKZ9	4	415	8.5	157	37
Q9brh3 homo sapien	Q9BRH3	4	276	8.5	157	8
Ω	Q9TU53	0	3620	8.5	158	5
Q8qzy7 mus musculu	Q8QZY7	11	926	8.6	158.5	
070244 rattus norv	070244	11	3623	8.7	160	3
Q8uvq9 gallus gall	Q8UVQ9	13	936	8.7	161.5	3
0	Q8UVR0	13	919	8.7	161.5	31
	Q9NQS4	4	1013	8.8	162	30
homo sapi	043897	4	1013	8.8	162	29
	057382	13	1019	8.9	165	8
Q62381 mus musculu	Q62381	11	1013	8.9	165	27
rat	Q9QX38	11	921	9.1	168	8
7 gall	Q9DER7	ш З	1008	9.1	169	25
homo	060494	4	3623	9.4	174.5	24
	Q9H2E1	4	704	9.5	176	23
homo	Q96IH5	4	644	9.5	176	22
7	096190	4	609	9.5	176	21
ratt	Q9Z135	11	241	9.8	181	0
mus	Q9WVM6	11	1012	9.9	183	19
_	Q9Y6L7	4	1015	10.0	185	8
Q9uq00 homo sapien	Q9UQ00	4	926	10.0	185	17

ALIGNMENTS

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RESULT
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                                                                                                                                                                                                                                                                                                         PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 345 AA; 38886 MW;
                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1859631; Pdgfc.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00042; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SWISS-WEBSTER/NIH;
MEDLINE-20417814; PubMed-10960785;
Ding H., Wu X., Kim I., Tam P.P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-UN-2002 (TrEMBLrel. 21, Last annotation
Platelet-derived growth factor C.
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EMBL; AF286725; AAF91483.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                       0,
                                                                                                                                                                                    Score 1819; DB 11;
Pred. No. 6.9e-160;
0; Mismatches 4;
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Pred. No. 1.4e-162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                               FA1486BED6D362F8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Sim
Matches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1
SEQUENCE 345 AA; 38734 M
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Q9EQX6;
01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence up
Ol-UN-2002 (TrEMBLrel. 21, Last annotation
Spinal cord-derived growth factor.
RSCDGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21092670; pubMed=11162582;
Hamada T., Ui-Tei K., Imaki J., Mi
"Molecular Cloning of SCDGF-B, a N
SCDGF/PDGF-C/fallotein.";
Biochem. Biophys. Res. Commun. 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AB033830; BAB19969.1; -.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=WISTAR;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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                                                                                        GRWCGSGTVPGKQTSKGNHIRIREVSDEYEPSEPGFCIHYSIIMPQVTETTSPSVLPPSA
                                                                                                               GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEDGFCIHYSIIMPQVTETTSPSVLPPSS
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LSLDLLNNAVTAFSTVEELIRFLEPDRWQIDLDSLYKFTWPLLGKAFLYGKKSKAVNLNL
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96.8%;
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Pred. No. 3.2e
5; Mismatches
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Sciurognathi; Muridae;
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a Novel Growth
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                                                                                                                                                                                                                                                                                                                                                              DB 11;
3.2e-158;
nes 6;
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Q SUSTINE REPORT OF THE REPORT
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C -!- SIMILARTY: CONTAINS 1 CUB DOMAIN.

R EMBL; AF091434; AAF00049.1; -. EMBL; AF260738; AAK51637.1. -. InterPro.
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                                                                                                                                                                                Query Match
Best Local S
Matches 300
                                                                                                                                                                                                                                                                     InterPro; IPRO00859; CUB_domain.
InterPro; IPRO00972; PD_growth_factor.
Pfam; PPO0431; CUB; 1.
Pfam; PPO0341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; DDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0178; PDGF_2; 1.
SEQUENCE 345 AA; 39029 MW; CDE9E51F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20317014; PubMed-10858496; Hamada T., U1-Tei K., Miyata Y.; "A novel gene derived from developing member of the PDGF/YEGF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Secretory growth factor-like protein FALLOTEIN (SPINAL growth factor) (Platelet-derived growth factor C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL22;
01-MAY-2000
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor) (
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                                                                                       Y.J., Lee R.K.K.,
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PREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL
                     PKFPHTYPRNMVLVMRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEEPSDGSVL 120
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growth
                                                                                                                                                                                                     90.2%;
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                                                                                                                                                                                27;
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Pred.
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                                                                                                                                                                                                                                                                       CDE9E51F40633E78 CRC64;
                                                                                                                                                                                                     1667;
No. 7
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Best Local S
Matches 299
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-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AF244813; AAF80597.1; --
InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM000111; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                        Backstrom G., Hellstrom M., Bostrom Betsholtz C., Heldin C.-H., Alitalo "PDGF-C is a new protease-activated receptor.";
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PROSITE; PS50278; PDGF_2;
SEQUENCE 345 AA; 39043
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Mammalia; Eutheria;
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01-0CT-2000 (TrEMBLrel 15, Las
01-JUN-2002 (TrEMBLrel 21, Las
Platelet-derived growth factor
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                        GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                        PKFPHTYPRNMVLVMRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
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Primates;
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MW;
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tor C.
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Pred. No. 1
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, Ostman A., Eriks
gand for the PDGF
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ies 18;
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Murinae; Rattus

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RESULT 7
Q9EQT1
ID Q9EQT1
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Best Local S
Matches 277
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01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
SFORMERCE 345 AA; 38940 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WHITE LEGHORN; TISSUE-SPINAL CORD;
MEDLINE-20317014; PubMed-10858496;
Hamada T., U1-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords,
member of the PDSF/PEGF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor
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FEBS Lett. 475:97-102(2000).
CONTAINS 1 CUB DOMAIN.
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; PF00341; PDGF; 1.
T; SM00042; CUB; 1.
T; SM00141; PDGF; 1.
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 PRELIMINARY;
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Pred. No. 3.4e
37; Mismatches
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 PRT;
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mes; Phasianidae; Phasiani
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1.4e-135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR000072; pD_gro
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1
SEQUENCE 370 AA; 42809 M
                                                                                                                                            Q9GZP0
Q9GZP0;
Q1-MAR-2001
01-MAR-2001
01-JUN-2002
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01-MAR-2001
01-MAR-2001
01-JUN-2002
Spinal-cord
RSCDGF-B.
                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed factor long form) (Platelet-derived growth factor D).
HSCDGF-B OR IEGF OR PDGFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21092670; PubMed=11162582;
Hamada T., UI-Tei K., Imaki J., Miyata
Hamada T. Cloring of SCDGF-B, a Novel
SCDGF/PDGF-C/fallotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Eukaryota; Metazoa;
 SEQUENCE FROM N.A.
                              NCBI_TaxID=9606;
                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                               LEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE
                                                                                                                                                                                                                                                                                                FKRRGKAKNMALVDIQLDHHERCDCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                VEDILKYFNPASWQDDLENLYMDTPRYRGRSY-HERKSK-VDLDRLNDDVKRYSCTPRNH
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                                                                                                                                                                                                                                                                                                                                 -KTGVKGLHKSLTDVALEHHEECDCVC
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51; Conservative
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
derived growth factor-B.
                                                                                                                                                                                                                  PRELIMINARY;
                                                                              (Human)
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a; Chordata;
                                              Chordata;
Primates;
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2; Mismatches
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                                              Craniata; Vo
Catarrhini;
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Growth
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                                                                Vertebrata; Euteleostomi,
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                                                 Hominidae;
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A Glese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Veri
A Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets Shimkets R.A., Rothberg J.M., Lichenstein H.S.;

T "PDGF D, A Novel Protease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
C -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
C SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AB033832; BAB18903.1; -.
R EMBL; AF336376; AA639287.1; -.
R EMBL; AF335584; AA639287.1; -.
R EMBL; AF335584; AAK38840.1; -.
R EMBL; AF335584; AAK38840.1; -.
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Best Local Similarity 45.3

Matches 148; Conservative
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PROSITE;
PROSITE;
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"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/PDGF-C/fallotein.";
Biochem. Biophys. Res. Commun. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergsten E., Uutela M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=IRIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alitalo K., Eriksson
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ubmitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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                                                                              PGFCIHYSII---MPQVTETT------SPSVLPPSSLSLDLLNNAVTAFST
                                                                                                                                                                                                                                                                                          LEDPEDDICKYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                           EQNGVQD-PRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFG
SVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--
                                                                                                                                                                                                                                                                                                                                                                ESNHLTDLYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLYFDNQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Biol. 3:512-516(2001)
                                                      VEDLLKYFNPESWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNY
                                                                                                                                                          PGFKIYYSLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDT
                                                                                                                                                                                                                                                               LEEAENDICRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01180; CUB; 1.
PS0278; PDGF_2; 1.
PS00430; TOWB_DEPENDENT_REC_1; UNKNOWN_1.
370 AA; 42848 MW; D387F485E7BB7674 CF
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45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 752; DB . Pred. No. 3.7e-59; Mismatches,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
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Wu Q.Y.,
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B., Shimkets J.,
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RESULT 10
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Best Local
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Q9BWV5;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2001) to the -!- SIMILARITY: CONTAINS 1 EMBL; AY027518; AAK20082.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
PROSITE; PS00430; TONB_DEPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1
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InterPro; IPR000072; PD_growth_
InterPro; IPR000531; TonB_boxC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2001 (TrEMBLrel. 17, I
01-JUN-2002 (TrEMBLrel. 21, I
Iris-expressed growth factor
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                                                                                                                                                         KYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI 162
                                                    MALVDIQLDHHERCDCIC
                                                                   KSLTDVALEHHEECDCVC
                                                                                                                                                                                                              LEDFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDTVEDLLKYFN
                                                                                                                                                                                                                                                                                                                                                RHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKRRGRAKTMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGH
                                                                                                      LANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKT
                                                                                                                                RTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--
                                                                                                                                                                                                                                         I---MPQVTETT----
                                                                                                                                                                                                                                                                 RYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSL
                                                                                                                                                                                                                                                                                                                      RRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KTGVKGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                                                                                                                                                                           PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the
                                                                                                                                                                                                                                       -----SPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e EMBL/GenBank/DDBJ
CUB.DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
r short form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                       Score 750.5; DB 4
Pred. No. 4.9e-61;
8; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                  -KTGVKGLH
                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                   264
                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337
                                                                                                                                  321
                                                                                                                                                                                                                                        204
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Q92517 Q92517;

PRELIMINARY;

PRT;

370

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RESULT
Q9D1L8
ρy
                                                                                                                                                                                                                                                               Вр
                                                                                                                                                                                                                                                                                       Q
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                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 151;
                                                                              Q9D1L8
Q9D1L8;
Q9D1L8;
Q1-JUN-2001 (TrEMBLrel. 1'
Q1-JUN-2001 (TrEMBLrel. 1'
Q1-JUN-2002 (TrEMBLrel. 1'
Q1-JUN-2002 (TrEMBLrel. 2'
Q1110003109Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001
01-DEC-2001
01-JUN-2002
                                  Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LaRocchelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimke Shimkets R.A., Rothberg J.M., Lichenstein H.S.; "PDGF D, A Novel Protease-Activated Growth Factor.";
                                                                      PDFGD OR 1110003109RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 370 AA; 42809 MW;
                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000072; PD_growth_factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00431; CUB; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1919035; Pdfgd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Cell Biol. 3:517-521(2001).
EMBL; AF335583; AAK38839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21231380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                               318
                                                                                                                                                                                                                                        296
                                                                                                                                                                                                                                                                 258
                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                         134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                              CSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC
                                                                                                                                                                                                                              CVPRKVTKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                                 VNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ
                                                                                                                                                                                                                                                                                                                            LPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKV 235
                                                                                                                                                                                                                                                                                                                                                              TSRTNQIKITFKSDDYFVAKPGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPSI
                                                                                                                                                                                                                                                                                                                                                                            QRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVW
                                                                                                                                                                                                                                                               VDLDRLNDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCT
                                                                                                                                                                                                                                                                                                               TDP-TLTADALDKTVAEFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK-
                                                                                                                                                                                                                                                                                                                                                                                                                WLRS-QEKTRIQLSFDHQFGLEEAENDICRYDFVEVEEVSESSTVVRGRWCGHKEIPPRI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                         RLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRASIKALRNAN----LRRDESNHLTDLYQREENIQVTSNGHVQSPRFPNSYPRNLLLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
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1 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                               Chordata;
                                   Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.48;
                                                                                               17,
17,
21,

    Created)
    Last sequence update)
    Last annotation update)
    factor D.

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                                                                                              Last sequence update)
Last annotation update)
                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 746.5; I
Pred. No. 1.2e
63; Mismatches
                                               Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9E80B4CF6813BFBE CRC64;
                                                                                                                                                  290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2e-60;
nes 102;
                                                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang M., Ve.
B., Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                               364
                                                                                                                                                                                                                                      339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
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                                                                                                                                                                                                                                                                                                                                                                                        VSqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus.
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                                                                                                                                                                                                                                                                                       295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                               317
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RESULT 12
Q8QFX6
ROCCOC DE DE AC
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                       Q8QFX6
Q8QFX6;
Q1-JUN-2002
01-JUN-2002
01-JUN-2002
                          Eukaryota; Metazoa;
Actinopterygii; Neop
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J. Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T. Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Satok H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
           Cyprinidae; Dan:
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000859; CUB_domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T. Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                          Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                          Neuropilin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01180; CUB; 1. PROSITE; PS50278; PDGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK003359; BAB22735.1; MGD; MGI:1919035; Pdfgd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 CUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                        302
                                                                                                                                                                                                                                                          244
                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                      VKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC
                                                                                                                                                                                                                                                                       TKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHEECDCVC
                                                                                                                                                                                                                                                                                                                                                                                     TADALDKTVAEFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK-VDLDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNH 139
                                                                                                                                                                                                                                                                                                                      NDDVKRYSCTPRNHSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCTCSSGKT
                                                                                                                                                                                                                                                                                                                                        KEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKV
                                                                                                                                                                                                                                                                                                                                                                                                                   SLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKITFKSDDYFVAKPGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPSITDP-TL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKTRIQLSFDHQFGLEEAENDICRYDFVEVEEVSESSTVVRGRWCGHKEIPPRITSRTNQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                         (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 AA;
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                           Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.7%;
46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                          Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 660;
Pred. No. 8
                                             Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 8.56
3; Mismatches
                                                        Craniata;
                                                                                                                                                                           .PRT;
                                                                           (Zebra danio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14214509E6717D4B CRC64;
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                                                                                                         sequence up annotation
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                                             Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse
                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
1.5e-53;
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                                                                                                                           update)
                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SPSVLPPSSL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukuda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ţ.,
                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                                                                                                                                                                                                      301
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RESULT
057658
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                       057658;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun I "Neuropilin-1 is required for normal vascular development and mediator of VEGF-dependent angiogenesis in zebrafish."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY064213; AAL40862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               057658
                                                      PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 3.
SMART; SM00179; EGF_CA; 1.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                               EMBL; U75331; AAC02259.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                    Gene 248:233-243(2000).
                                                                                                                                                                                                                                                                   MEDLINE=20267865; PubMed=10806368; Reynolds S.D., Zhang D., Puzas J.E. Reynolds P.R.; "Cloning of the chick BMP1/Tolloid
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae;
                                 PROSITE;
                                                                                                                                              InterPro;
                                                                                                                                                          InterPro;
                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                      MEROPS; M12
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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                                                                                                                                    InterPro;
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                                                                                                                                                                                interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                      morphogenetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGYPVSYYPSQKCIWVITAPGPNQRILINFNPHFDLEDRE---CKYDYVEVRDGVDENGQ
                                                                                                 PF01400; Astacin; PF00431; CUB; 3. PF00008; EGF; 1.
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; PS00010; ASX_HYDROXYL; 1.
; PS01180; CUB; 3.
; PS01186; EGF_2; 1.
; PS01187; EGF CA; 1.
; PS00142; ZINC_PROTEASE; U
                                                                                                                                 o; IPRO01506; Astacin.
c; IPRO00152; Asx_hydroxyl.
c; IPRO00859; CUB_domain.
c; IPRO00561; EGF-like.
c; IPRO01881; EGF_Ca.
c; IPRO00130; Zn_MTpeptdse.
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mang D., Puzas J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasian!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102492 MW;
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Last annotation update)
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Pred. No. 1.2e
31; Mismatches
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.2e-09;
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                                                                                                                                                                                                                                                                                         R.J.,
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Best Local
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                                                                                                                                                  Q91925;
Q91925;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99JM4;
Q99JM4;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2002
Lin J., Maeda R., Ong R., Kim J., Kung H., Maeno M.; "Xtld, a Xenopus homolog of dorso-ventral plantity g modifies tissue phenotypes of the ventral mesoderm." Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databa
                                                                                             Eukaryota; Metazoa;
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL; BC006027; AAH06027.1; MGD; MGI:1859631; Pdgfc. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium-binding; EGF-like domain; NON_TER 1 1
                                                                                                                             Xtld protein.
                                                                                                                                        01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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                                           TISSUE=EMBRYO;
                                                                         NCBI_TaxID=8355;
                                                                                     Xenopodinae;
                                                                                                                  Xenopus laevis (African
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                                                                                             Batrachia;
                                                                                                                                      6 (TrEMBLrel.
6 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                         34 AA; 3618 MW;
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                                                                                     Xenopus
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Rodentia;
                                                                                                          Chordata;
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                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                        10.4%;
100.0%;
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                                                                                                                                                                                                                                                                                                  Score 192;
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                                                                                                                                                                                                                                                                                                                       F4AB6A3A414AED9E CRC64;
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Mismatches
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                                                                                                                                                                                   PRT;
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PROSITE; PS01180; CUB; 5.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01042; ZINC_PROTEASE; UNICALCium-binding; EGF-like domain; GSEQUENCE 977 AA; 110199 MW; 4D71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01400; Astacin; 1.
Pfam; PF00441; CUB; 5.
Pfam; PF00008; BGF; 2.
PRINTS; PR00480; ASTACIN.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
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                                                                                   646 LTSDSKLHGKFCGS-ELPAVITSQYNNMRIEFKSDNTV-SKKGF 687
                                                                                                                                                                      114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                            ; ZINC_PROTEASE; UNKNOWN_1.

EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
A; 110199 MW; 4D7D2E37C64FDF1F CRC64;
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A; Residues: 1-370 < HAM>
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Result No.

Score

754 754 759 190 183.5 183.5 181 174.5 160 160 153 147.5 147.5 144

Minimum DB Maximum DB

seq seq

Post-processing:

Database

Perfect score: Sequence:

Title:

9

Scoring table:

Searched:

ALIGNMENTS

A:Gene: scdgf-B
A:Gene: scdgf-B
F;1-17/Domain: secretory signal sequence #status predicted <SIG>
F;18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F;18-370/Region: CUB domain #status predicted
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial
F;274-308/Region: conserved motif #status predicted spinal cord-derived growth factor-B precursor - rat C; Species: Rattus norvegicus (Norway rat) C; Species: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001 C; Accession: JC7592 R; Hamada, T; U1-Tei, K; Imaki, J; Miyata, Y. Biochem. Biophys. Res. Commun. 280, 733-737, 2001 Biochem. Biophys. Res. Commun. 280, 733-737, 2001 A; Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to A; Reference number: JC7591; MUID:21092670; PMID:11162582 A; Contents: Fetal brain A; Accession: JC7592. A;Cross-references: DDBJ:AB052170 C;Genetics: FKRRGKAKNMALVDIQLDHHERCDCIC -KTGVKGLHKSLTDVALEHHEECDCVC SVNLREELKLINAVFFPRCLLVQRCGGNCGCGTLNWKSCTCSSGKTVKKKHEVLKFEPGH SVSIREELKRTDT1FWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--LEDPEDDICKYDEVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIREVSDEYEPSE 153 VEDILIKY FNPASWQDDLENLYMDT PRYRGRSY - HERKSK - VDLDRLNDDVKRYSCT PRNH Conservative 40.8%; 62; Score 754; DB Pred. No. 1.4e 62; Mismatches 339 DB 2; 1.4e-55; hes 86; ... Length 370; Indels 28; Gaps 277 255 219 195 SCDGF/PDGF 10;

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Gene 134, 257-261, 1993

A;Title: Cloning and expression of cDNA encoding Xenopus laevis both A;Reference number: JC2218; MUID:94085787; PMID:8262384

A;Reference number: JC2218

A;Accession: JC2218

A;Molecule type: mRNA

A;Residues: 1-707 <MAE>

A;Cross references: GB:L12249; NID:9406540; PIDN:AAA16313.1; PID:9-C:Comment: This protein induces ectopic cartilage formation in vivo C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C;Superfamily: procollagen C-endopeptidase; astacin hydrolase; metaller: 93-284/Domain: astacin homology <AST>
F:285-397/Region: complement 1r/1s-like repeat

F:398-510/Region: complement 1r/1s-like repeat
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A;Title: Molecular cloning of SCDGF-B, a novel growth fac
A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Accession: JC7591
A;Molecule type: DNA
A;Residues: 1-370 <HAM>
A;Cross-references: DDBJ:AB033832
C;Genetics:
                                                                                                                                                                                                                                                                                                        N;Alternate names: bone morphogenic protein 1
C;Species: Xenopus laevis (African clawed fro
C;Date: 30-Sep-1993 #sequence_revision 20-Aug
C;Accession: JC2218
R;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.;
Gene 134, 257-261, 1993
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F;1-17/Domain: secretory signal sequence #status predicted <SIG>
F;18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F;52-170/Region: CUB domain #status predicted
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow F;272-370/Region: conserved motif #status predicted
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_rev
C;Accession: JC7591
R;Hamada, T; U1-Tei, K.; Imaki,
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Pred. No. 1.7e-55;
9; Mismatches 92;
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20-Aug-1994 #text_change
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NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE-

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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MP
F;23-823/Product: a stacin homology <AST>
F;130-321/Domain: astacin homology <CIR1>
F;322-431/Domain: Clr/Cls repeat homology <CIR2>
F;322-431/Domain: Clr/Cls repeat homology <CIR2>
F;325-544/Domain: Clr/Cls repeat homology <CIR2>
F;51-887/Domain: EGF homology <EGF>
F;591-700/Domain: Clr/Cls repeat homology <CIR3>
F;591-700/Domain: Clr/Cls repeat homology <CIR3>
F;591-700/Domain: Glr/Cls repeat homology <CIR3>
F;38-752/Region: histidine-rich
F;91,142,332,363,399/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,6
F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F;167-914/Active site: Cln #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeating controls; alternative splicing; beta-hydroxyasparagine; bone; calcium; du C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; du C;Keywords: alternative splicing; beta-hydroxyasparagine; but beta-hydroxyaspa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-702,'EKRPALOPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1;
R·Takahara, K.; Lyons, G.E.; Greenspan, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M. Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular A; Reference number: A37278; MUID:89072730; PMID:3201241
A; Accession: A37278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:BMP1; BMP-1
A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K;Takahara, K.; Lyc
J. Biol. Chem. 269,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Bone morphogenetic protein-1 and a mammalian tolloid A; Reference number: A58788; MUID:95096114; PMID:7798260
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N;Alternate names: bone morphogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 703-823 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Accession: A37278; A58788
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    Matches
                                        Query Match
Best Local
                                                                                                                                                                                                 214/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF
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                                        Similarity
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    Conservative
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                                                                                                                                                         erythro-beta-hydroxyasparagine (Asn) #status
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                                        10.3%;
36.0%;
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    20;
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                                    Score 190; DB 1
Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 191; DB 2;
Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.J.; Mitsock, L.M.; Whitters,
    Mismatches
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e (Asn) (covalent) #status
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                                                                            DB 1;
    48;
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                                                                            Length
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    Indels
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    28;
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    Gaps
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A; Gene: GDB:BMP1
A; Cross-references: GDB:125
A; Map position: 8p21-8p21
C; Function:
A; Description: catalyzes hy
C; Superfamily: procollagen
C; Keywords: alternative spi
F; 1-22/Domain: signal seque
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A; Cross-refe
C; Genetics:
                       C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JH0466; J00948
R:Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  procollagen C-endopeptidase (EC 3.4.24.19) precursor,
N:Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens /man\'
                                                                                                                    JQ0948
A5 ant:
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A; Residues: 1-730 <WOZ>
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Best Local
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                                                                                                                                                                                                                                                     PSVLPP 178
                                                                                                                                                                                                                                                                                        LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF-----
                                                                                                                                                                                                                                                                                                                       -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTS 172
                                                                                                                                                                                                                                                                                                                                                                NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                                                                                                                                                                   NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SIIMPQVTETTSPSVLPPSSLSLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHFFSVLEGAGDRHS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG
                                                                                                                    precursor - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Conser
       A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site: erythro-beta-hydroxyasparagine (Asn) #status predicted
       antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB:125203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:M22488; NID:g179499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.9%;
       candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celeste, A.J.; Mitsock, L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMIM: 112264
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 183.5;
Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
       for
       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: AAA51833.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3e-07;
       neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
     recognition molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splice form BMP1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID: g179500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and activities
                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.J.; Kriz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160
     has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.W.;
     homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He
A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication F;1-22/Domain: signal sequence #status predicted <SIG>F;23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predi F;130-321/Domain: astacin homology <ASTP: F;322-431/Domain: Clr/Cls repeat homology <CIR1>F;435-544/Domain: Clr/Cls repeat homology <CIR1>
                                                                                                                                                  A;Cross-references:
A;Map position: 8p2:
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: Asyluter R:Wozney, J.M.; Rosen, V.; Celeste R:Wozney, J.M.; Rosen, V.; Celeste R:Wozney, J.S.28-1534, 1988 Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Ji
A; Accession: JH0466
A; Molecule type: mRNA
A; Residues: 1-927 <TAL
                                                                                                                                                                                                                                A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: A37278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                            A; Gene: GDB: BMP1; BMP-1
                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 703-986 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                              R;Takahara, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVTE--TTSPSVLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-927 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                       8p21-8p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                           GDB:125203;
                                                                                                                                                                                                                                               GB:L35279;
                                                                                                                                                                                                                                                                     <TAK>
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F;22-927/Product: A5 antigen #status predicted <A5A> F;27-138/Domain: C1r/C1s repeat homology <C1R1> F;147-262/Domain: C1r/C1s repeat homology <C1R2> F:274-424/Domain: discoidin I amino-terminal homology F;274-424/Domain: discoidin I amino-terminal homology F;430-584/Domain: MAM homology <MAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: tadpole, brain
A;Note: this protein has motifs homologous to complement components C1r and C1s and t
C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal
C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-termina
C;Keywords: duplication; glycoprotein; transmembrane protein
C;Keywords: signal sequence #status predicted cSIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01260.1; PID:g222963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861-883/Domain: transmembrane #status predicted 150,261,300,523,844/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                     50 VTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV
                                                                                                                                                                                                                                                        IKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE----CKYDYV 87
ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFA----PKMQEIV--LEFESFELEADS
                                                                                                                               EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP 145
                                                                                                                                                                    EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JH0466;
                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%;
30.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUID:91337458; PMID:1908252
                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                         PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 183.5; DB 1;
Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        65;
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                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        927;
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
198
                                                                                                                                                                                                                                                                                                                     109
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J. Biol. Chem. 269, 32572-32570, 1377
J. Biol. Chem. 269, 32572-32570 and a mammalian to A;Title: Bone morphogenetic protein-1 and a mammalian to A:Reference number: A58788; MUID:95096114; PMID:7798260 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloi N;Alternate names: bone morphogenic protein 1, tolloid-like C;Species: Homo sapiens (man) C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_cha C;Accession: A37278; B58788 A; Molecule type: mRNA A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ' A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; Lyons, G.E.; Greenspan, D.S. 269, 32572-32578, 1994 A37278; MUID:89072730; PMID:3201241 Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, NID: g619860; formation: molecular PIDN: AAC41710.1; <WOZ> #text_change 16-Jul-1999 tolloid-like d-like splice tolloid clones PID:g619861 PID:g179500 and homologue (mTld) splice form form are æ Σ huma

OMIM: 112264

predic

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C; Species: FC; Date: 16-GC; Accession: R; Kozyraki, Blood 91, 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision
C;Accession: I49540
                                                                                                                       RESULT
T09456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procollagen
C;Species: M
                                                                       intrinsic factor-B12 receptor Cubilin precursor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-19
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              A;Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I49540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Fukagawa, M.;
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ion.
                                                         Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: procollagen C-endopeptidase; astacin; Keywords: hydrolase; metalloproteinase; zinc; Keywords: hodrolase; metalloproteinase; zinc; 135-326/Domain: astacin homology <AST>; 556-592/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: Bmp-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,
213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707-742/Domain: EGF homology <EG2>
747-856/Domain: Clr/Cls repeat homology
860-973/Domain: Clr/Cls repeat homology
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                   712-747/Domain: EGF homology <EG2>
218,222,228,277/Binding site: zinc (His, His, His,
                                                                                                                                                                                                                                                                                                                                                                                                                   596-705/Domain: Clr/Cls repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                                                                                                                                                                                                                                                                                                                                                                       Active site:
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                                                                                                                                                                                   660
                                                                                                                                                                                                               114
                                                                                                                                                                                                                                              604
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            The human
                           l, R.; Kristiansen, M.; Silahtaroglu, 3593-3600, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY
                                                                                                                                                                                   LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF
                                                                                                                                                                                                               -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY
                                                                                                                                                                                                                                                                           NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE-
                                                                                                                                                                                                                                              NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG
                                                                                                                                                                                                                                                                                                           Similarity 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-991 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                           T09456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175-183,
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clr/Cls repeat
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                                                                                                                                                                                                                                                                                                                                                                    Glu #status predicted
            intrinsic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:L24755;
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                                                                                                                                                                                                                                                                                                                      9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hogan,
            factor-vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID: g439606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <EG1>
                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology
                                                                                                                                                                                                                                                                                                                                                                                                                 homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 181; DB 1; Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                           Pred. No. 7.2
5; Mismatches
                                                                                                                                                                                                                                                                                                                      Score 181; DB 2;
Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <C1R5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <C1R3>
                                                                                                                                                                                                                                                                                                                                                                                                                   <C1R>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones,
            B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAA37306.1;
                                         A.; Hansen,
           receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                       human
                                                                       #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 986
                                                                                                                                                                                                                                                                                                                                    Length 991
                                                                                                                                                                                                                                                                                                                                                                                    Tyr) #status
                                                                                                                                                                                                                                                                                                           Indels
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            cubilin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-1
                                         c.;
                                                                                                                                                                                                               160
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                                                                                                                                                                                   705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID: 9439607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clr/Cls repeat homology;
                                         Jacobsen, C.;
                                                                       02-Aug-2002
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C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; F;1-20/Domain: signal sequence #status predicted <SIG> F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status pr. F;133-164/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology C;Keywords: receptor; vitamin B12 uptake F;1-24/Dumain; signal sequence #status predicted <SIG>F;25-3623/Product: intrinsic factor-B12 receptor #status predicted
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A; Residues: 1-3623 <K
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A; Residues: 1-3623 < MOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T08618
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EGF homology <EGF>
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Pred. No. 1.3e-05;
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                                                                                                                                                                                                                                                                                                                    Score 160;
Pred. No. 0.
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A Map position: 7q21.3-7q22
C; Superfamily: C1r/C1s repeat homology
C; Keywords: extracellular protein; glycoprotein; pyrog
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-449/Product: #status predicted <MAT>
F; 37-146/Domain: C1r/C1s repeat homology <C1R1>
F; 159-270/Domain: C1r/C1s repeat homology <C1R2>
F; 26/Modified site: pyrrolidone carboxylic acid (Gln)
F; 29,431/Binding site: carbohydrate (Asn) (covalent) #
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R;Takahara, K.; Kess
J. Biol. Chom
A;Title: The Drosphila dorsal-ventral patterning gene tolloid A;Reference number: A39288; MUID:92034970; PMID:1840509 A;Accession: A39288 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1057 <SHID A;Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PIC;Genetics: A;Gene: FlyBase:tld
                                                                                                                                                                                                                                                dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit C;Species: Drosophila melanogaster C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: A39288
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A;Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, A;Reference number: A55362; MUID:95014462; PMID:7523404
A;Accession: A55362
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C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C;Accession: A55362
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                                                                                                                                                                                                      R;Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B. Cell 67, 469-481, 1991
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A; Residues: 1-449 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTLTTPNWPESDYPPGISCSWHIIAPPDQV-IALTF-EKFDLE--PDTYCRYDSVSVFNG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKYHE----VLQLRPKTGVKGLHKSLTDVALEHHEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFKSDAALTAKGFSA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PQVTETTSPSV-LPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFTDFTLEDYFGSQCVDFVEI-RDGGYE-TSPLVG---IY--CGSVLPPTIISHSNKLWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%;
34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----YWDGS--STGCGGN----LTTPTGVLTSPNYPM 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 158; DB 2; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                              (EC 3.4.24.-) - fruit fly (Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335
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<SIG>
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s predicted
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                                                                                                                                                                                   related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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C; Species: Xenopus laevis
C; Date: 22-Oct-1999 #seque
C; Accession: T30337
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F;747-782/Domain: EGF homology <EG2>
F;747-782/Domain: Clr/Cls repeat homology <Clr4>
F;787-896/Domain: Clr/Cls repeat homology <Clr4>
F;990-1013/Domain: Clr/Cls repeat homology <Clr5
F;221,225,231,280/Binding site: zinc (His, His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: FlyBase:FBgn0003719
C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls r C;Keywords: duplication; hydrolase; metalloproteinase; zinc F;136-329/Domain: astacin homology <ASTD
F;352-464/Domain: Clr/Cls repeat homology <CIR1>
F;468-578/Domain: Clr/Cls repeat homology <CIR2>
F;585-620/Domain: EGF homology <EGI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March:
A:Description: cDNA cloning of ovochymase,
A:Reference number: Z20829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T30337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T30337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;222/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: Ī-1524 <YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyprotein - African clawed
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
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613
                                      215
                                                                              553
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                                                                                                                                                               495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHERV----VTISGNGSIHSPKFPHTYP
                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                          GMIYSPNYPDPYPRLKTCSW-IIEAPENHIVKLKFED-FNVEYGHG--CIYDAVEVYDGA 494
                                      LYKPTWQL
                                                                            DTPTISMLHPRAIALDVCGMAPMTPKWWLPRIVGGEEASPNSWPWQVQIFFLRTFHCEGA 612
                                                                                                                                                                                                                                                                                GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EEP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTVPGKQTSKGNHIRIRFVSD 147
IISPQWIL 620
                                                                                                                     ETTSPSVLPPSSLSLDLLNNA-VTAFSTLEELIRYLEPD----RWQVDL----
                                                                                                                                                           EEKQLIARLCGY-TLPLPISSPENTMLIRFKTD-MENSYPGFKVKFSFVPKEKQFSLPVD 552
                                                                                                                                                                                                    SDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQ------VT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLPPNIKT-RSNOMYIRFVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDKECVWRITAPD-NHQVALKF-QSFELE--KHDGCAYDFVEIRDGNHSDSRLIGRFCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSDGSVLGRWCGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSGEVITTQTSRMLLNYVNRNAAKGYRGFK-ARFEVVCGGDLKLTKDQSIDSPNYPMDYM 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                             L Similarity
54; Conser
                                                                                                                                                                                                                                                                                                                             Conservative
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                                      222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.3%;
                                                                                                                                                                                                                                                                                                                                              8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (African clawed frog)
ence_revision 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566
                                                                                                                                                                                                                                                                                                                             34;
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                                                                                                                                                                                                                                                                                                                                            Score 147.5;
Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 153;
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b, a cl
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73;
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                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                   214
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Ra-reactive factor (EC 3.4.21.-) 2 N;Alternate names: mannose binding C;Species: Homo sapiens (man)

precursor protein-associated

serine proteinase

2 (MASP-2)

RESULT 14 A59271

Db QΥ B QУ DЬ

В Š

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Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins found in a bactericidal A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Accession: JN0883
A;Molecula to the customers of the Cls family of complement proteins found in a bactericidal A;Accession: JN0883
                      A; Experimental source: liver C; Comment: This is a serum b
C;Genetics
                                                                        A;Molecule type: mRNA
A;Residues: 1-234,'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699 <TAK:
A;Cross-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; F;1-15/Domain: signal sequence #status predicted <SIG> F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT> F;19-134/Domain: Clr/Cls repeat homology <ClR1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I54763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Molecular characterization of a novel serine protease A; Reference number: I54763; MUID:94289349; PMID:8018603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: mannose binding
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A;Cross-references: GDB:6071500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end of the mature protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-699 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ra-reactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Accession: I54763; JN0883; Sato, T.; Endo, Y.; Matsushint. Immunol. 6, 665-669, 1994
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300-361/Domain: complement factor H répeat homology <FH1>
366-430/Domain: complement factor H répeat homology <FH2>
445-679/Domain: trypsin homology <TRY>
72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;142-180/Domain: EGF homology <EGF>
;184-293/Domain: C1r/C1s repeat homology <C1R2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A5927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 SDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 TDREEHGPFCGK-TLPHRIETKSNTVTITFVTDE-SGDHTGWKIHYT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; translated
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A;Map position: 3q27-3q28 (;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; F;1-17/Domain: signal sequence #status predicted <SIG> F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT> F;19-135/Domain: Clr/Cls repeat homology <CIR1>
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F:143-181/Domain: C1r/C1s repeat homology <C1R2>
F:185-294/Domain: C1r/C1s repeat homology <CFH1>
F:361-362/Domain: complement factor H repeat homology <FH1>
F:367-432/Domain: complement factor H repeat homology <FH2>
F:437-432/Domain: trypsin homology <TRY>
F:449-178-407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:49,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:49,178-40,178-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-5
Search completed: April 29, Job time: 19.5 secs
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Neuropilin-1 precursor (A5 protein) (A5 antigen).
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Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
"The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";
Neuron 7:295-307(191).
                                                                                                                                                                                                                                                                                                            XENLA
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                            SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITIC BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS. SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
                                                                             FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS
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 DOMAINS
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Signal;
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BMP1_HUMAN
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PROSITE; PS00740; MAM; 1; 1.

PROSITE; PS01180; CUB; 2; 2.

PROSITE; PS01285; FA58C_1; 2.

PROSITE; PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0020; MAMDOMAIN SMART; SM00042; CUB; 2. SMART; SM00231; FA58C; 2. SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by anc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00629; MAM; 1. Pfam; PF00754; F5_F8_type_C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                            EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIREVSDEYFPSEPGFCIHYSIIM--P
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                                                  ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFA----PKMQEIV-
                                                                    QVTE - - TTSPSVLP - - -
                                                                                         EVIDGDNANGQLLGKYCGK-TAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP
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STANDARD;
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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                                                                                                                                                                                    Score 183.5;
Pred. No. 2.
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CUB 1.
CUB 2.
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PRT;
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986
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p13497; Q13294; C. Ol-JAN-1990 (Rel. 13, Createu, 01-JAN-1990 (Rel. 40, Last sequence update, 15-JUN-2002 (Rel. 41, Last annotation update) Bone morphogenetic protein 1 precursor (EC 3.4. 'Procollagen C-proteinase) (PCP) (Mammalian tol
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahara K., Lyons G.E., Greenspan D.S.;

Bone morphogenetic protein-1 and a mammalian tolloid homologue
are encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";

J. Biol. Chem. 269:32572-32578(1994).

-!- FUNCTION: CLEAVES THE C-TERMINAL PROPERTIDES OF PROCOLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98160316; PubMed-9500680; Janitz M., Heiser V., Boettcher U., La "Three alternatively spliced variants bone morphogenetic protein-1."; J., Mol. Med. 76:141-146(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitte Kriz R.W., Hewick R.M., Wang E.A.; "Novel regulators of bone formation: molecular clones and activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95096114; PubMed=7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM BMP1-MEDLINE-89072730; Pubmed-3201241;
                                                                                                                                                                                                                                                                             Alternative splicing.
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND II. INDUCES CARTILAGE AND BONE FORMATION. CATALYTIC ACTIVITY: Cleavage of the C-terminal Ala-1-Asp in type I and II procollagens and at
                                                                                                                                                                                                                                                                                                                                                                                              ENDOPEPTIDASE ENHANCER PROTEIN.
ALTERNATIVE PRODUCTS: 7 isoforms;
here), BMP1-4, BMP1-5, BMP1-6 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93:5127-5130(1996).
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BMP1-7;
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EMBL; Y08725; CAA69975.1
EMBL; L35278; AAC41703.1
EMBL; L35279; AAC41710.1
PIR; A37278; A37278.
HSSP; P00736; IAPQ.
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PROSITE; PS001180; CUB; 5
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
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Pfam; PF00431; CUB; 5.
Pfam; PF01400; Astacin; 1.
PRINTS; PR00480; ASTACIN.
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SM00179; EGF_CA;
SM00235; ZnMC; 1.
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CUB 2.
CUB 3.
EGF-LIKE 3
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                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
DKDECSKONGGCODOCVNTEGSYEOGOR -> EKRPALOPP RGRPHOLKFRVOKNNRTPO (IN ISOFORM BMP1-1).
MISSING (IN ISOFORM BMP1-1).
QEYNPILKBEPOEVESLGETYDDEJIMHYARNTFSRGIFLDT IVPKYEVNGVKPPIGGR -> VLHSSLLLLSGGSRNGASFP CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
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(IN ISOFORM BMP1-4).

MISSING (IN ISOFORM BMP1-4).

AACGGFLTKLNGSITSPGWPKEYPPMKNCIWQLV

DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (IN
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BY SIMILARITY.
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J. Mol. [4]

TISSUE-Placenta; SEQUENCE FROM N.A. Science activities

242:1528-1534(1988).

(ISOFORMS

MEDLINE-96209868;

N.A.

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A.L., that

Prockop D.J Li S.W., TISSUE=Skin SEQUENCE FROM NCBI_TaxID=9606;

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protein-1

Natl. Acad. Sci. U.S.A.

is identical to the

protein

Eukaryota; Metazoa;
Mammalia; Eutheria;

Chordata; Primates;

TISSUE-Placenta;

U50330; M22488; Y08723;

AAA93462.1; AAA51833.1; CAA69973.1;

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RESULT
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Best Local
                                      !- COFACTOR: BINLS
!- COFACTOR: BINLS
!- ENZYME REGULATION: ACTIVITY 15 1.....
ENDOPEPTIDASE ENHANCER PROTEIN.
-!- TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MAT AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN MEMBRANOUS AND ENDOCHONDRAL BONE, SUBBUCOSA OF INT! OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Embryo;
MEDLINE-94229342; PubMed-8174772;
Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
"in the prosphila dorsoventral gene tolloid and encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).

-i- FUNCTION: CLEAVES THE C-TERMINAL PROPEDTIDES OF PROCOLLAGEN I, I:
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use
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                    Bone morphogenetic protein (Procollagen C-proteinase)
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16-OCT-2001
                           between
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMP1_MOUSE
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COPACTOR: BINDS 1 ZINC ION (BY COPACTOR: BEGULATION: ACTIVITY IN
                                                                                                                                                                                              AND II. INDUCES CARTILAGE AND BONE FORMATION. CATALYTIC ACTIVITY: Cleavage of the C-terminal Ala-|-Asp in type I and II procollagens and at
 European Bioinformatics Institute.
by non-profit institutions as 1
                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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40. Last annotation update)
c protein 1 precursor (EC 3.4.24.19) (BMP-1)
oteinase) (PCP) (Mammalian tolloid protein)
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MISSING. (IN ISOFORM BMP1-7).
D -> N (IN REF. 4).
R -> S (IN REF. 4).
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EAGCDHKVTSTSGTITSPNWDDKYPSKECTWAISSTGHR
VKLFEMEMDIESQPECAJDHLEVFDGRDAKAPVLGRECG
-> VLEGAGDRHSHLSGLELLLCPHALVDTVPAPPSALHGD
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SMART; S
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-PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY
                      NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG
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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT

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PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS001180; CUB; 5.
PROSITE; PS001010; ASX_HUDROXYL; 2.
PROSITE; PS001022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
GROWth factor; Cytokine; Repeat; Bone Growth factor; Cytokine; Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000561;
InterPro; IPR001881;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:88176;
NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00008; EGF;
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BY SIMILA
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BY SIMILARITY.
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                                                                                    38;
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30-MAY-2000 (Rel. 39, Creacc, 30-MAY-2000 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) 16-CCT-2001 (Rel. 40, Last annotation update) 16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Neuropilin-1 is expressed by endothelial and tumor cells isoform-specific receptor for vascular endothelial growth cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gagnon M.L., Bielenberg D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20183929; PubMed=10688880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Prostatic adenocarcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
 ALTERNATIVE PRODUCTS: 2 ISOFORMS; MEMBRANE-BOUND (SHOWN HERE)
AND SOLUBLE/SNRP1; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND
SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-
BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT
                                                                                                  FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS I SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRI
                                                                                     ISOFORM IS SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR NRP OR VEGF165R
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Matches 57
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-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
-!- SIMILARITY: CONTAINS 1 MAM DOMAIN.

This SWISS-PROT entry '-
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Pfam;
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PROSITE; PS01285; FA58C_1;
PROSITE; PS01286; FA58C_2;
PROSITE; PS00740; MAM_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00020; MAMDOMAIN
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                 Similarity
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Conservative
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                                                                            W-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

EFP -> GIK (IN SOLUBLE/SNRP1 ISOFORM).

MISSING (IN SOLUBLE/SNRP1 ISOFORM).

K -> E (IN REF. 1).

D -> H (IN REF. 2).
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                                                                     MW.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                            PROBABLE. PROBABLE.
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CUB 1.
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Indels
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WEDLINE=98188099; TISSUE-Breast SEQUENCE FROM "Neuropilin

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RESULT 6
TLD_BRARE
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dorsal-ventral patterning tolloid protein precursor (EC 3.4
DE (Mini fin protein)
N TOLLOID OR TLD OR MFN.
S Brachydanio rerio (Zebrafish) (Danio rerio).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos C Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
C Whent The Companio of the Companio of the Cyprinidae; Danio.
C Cyprinidae; Danio.
InterPro;
InterPro;
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                            InterPro;
InterPro;
                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                         EMBL; AF027596; AAC60304.1; HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98057457; PubMed-9395394;
Blader P., Rastegar S., Fischer N., Strael
"Cleavage of the BMP-4 antagonist chordin
Science 278:1937-1940(1997).
                                                           MEROPS; M12.016; -.
ZFIN; ZDB-GENE-990415-265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Development 126:3119-3130(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The role of tolloid/mini fin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zebrafish embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99307076; PubMed=10375503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND TISSUE SPECIFICITY
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                                                                                                                                                                                                                                              closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-somite stage, expressed in the developing tailbud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoietic system.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                 from inactive complexes.
TISSUE SPECIFICITY: During gastrulation,
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                           IPR001506; Astaci
IPR000152; Asx_hy
IPR000859;
IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION,
CUB_domain.
EGF-like.
                            Asx_hydroxyl.
                                                            tolloid
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PROSITE; PS010022; EGF_1; FALSE_NEG.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 2.

PROSITE; PS01142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01400; Astacin; 1.
PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 5.
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                              114
                                                             635
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LSSDSKLHGKYCGT-EVPEVITSQYNNMRIEFKSDNTV-SKKGFKAHF
                                                                                       NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                             -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY
                                                           NGTITTPGWPKEYPPNKNCVWQVVAPTQ-YRISMQF-EAFELEG--NEVCKYDYVEVRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SM00042; CUB; 5.; SM00181; EGF; 2.; SM00179; EGF_CA; 2.; SM00235; ZnMC; 1.
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                                                                                                                                      Similarity
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; EGF-like;
                                                                                                                         20;
                                                                                                                                                                                 BY SIMILARITY
BY
                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUB 3.
EGF-LIKE
                                                                                                                                      Score 174; DB 1 Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METALLOPROTEASE CUB 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN.
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                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Signal; Glycoprotein;
                                                                                                                                                      1;
                                                                                                                         35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
                                                                                                                                                    Length 1022;
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                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
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                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                             160
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                                                                                                                     Gaps
                                                           690
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RESULT 7

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PRINTS; PRO0020; MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOCENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLOF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.

-I- SIMILARITY: CONTAINS 2 CUB DOMAINS.

-I- SIMILARITY: CONTAINS 2 TYPE C DOMAINS.

-I- SIMILARITY: CONTAINS 2 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                        EMBL; AF016296; AAC53337.1; HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Neuropilin is a semaphorin III receptor."; Cell 90:753-762(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9QWJ9;
16-OCT-2001 (Rel.
                                         DOMAIN
DOMAIN
                                                                               CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ginty D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97433085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                              Pfam; PF00431; CUB; 2.
Pfam; PF00629; MAM; 1.
Pfam; PF00754; F5_F8_type_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRP1_RAT
                                                                                                        Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                   InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; FA58_C.
InterPro; IPR001092; HLH_basic.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolodkin A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropilin-1
                                                                   FRANSME
                                                                                                                                  PROSITE;
                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                  PS50060;
                                                                                                                                            PS00740;
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                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long
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Glycoprotein; 1
1 21
22 922
22 855
22 856
880
881 922
921 141
147 265
275 424
431 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9288754;
vengood D.V., Rowe E.G.,
                                                                                                                                  MAM_2;
                                                                                                                                              MAM
                                                                                                                                                          FA58C_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                          NN
  CUB 1.
CUB 2.
F5/8 TYPE
F5/8 TYPE
                                                                                                                      Neurone;
                                                     CYTOPLASMIC (POTENTIAL)
                                                                               NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cell growth factor
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                                                                                                                   Signal; Repeat; Receptor
                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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There are no re
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RESULT 8
NRP1_MOUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropilin, in the mouse nervous system.";

J. Neuropilin, in the mouse nervous system.";

J. Neuropilin, receptor involved in the development of the carcinon: receptor involved in the development of the carcinomascular system, in angiogenesis, in the formation of Certain Neuronal Circuits and in Organogenesis Outside the Nervous Certain in Mediates the Chemorepulsant activity of Semaphorins. It is in the Diates of the Chemorepulsant activity of Semaphorins. It is in the Diates of the Chemorepulsant of the Neuropell Signorm of Pof, the Vegf-165 in Increased vegf-165 in Increased Chemotaxis.

C. IT MAY REGULATE VEGF-INDICED ANGIOGENESIS (BY SIMILARITY).

C. IT SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

C. IT SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

C. IT SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                        "Developmentally regulated expression of a cell
                                                                                                                                                                                                                                                                                                 MEDLINE=96353149; PubMed=8748368;
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                        Neuropilin-1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                       P97333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRP1_MOUSE
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                  NRP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                             TISSUE=Embryonic brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    811
54
104
173
228
424
424
583
150
261
300
522
841
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Rodentia;
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BY SIMILARITY.
N-LINKED (GLCN.
N-LINKED (GLCN.
N-LINKED (GLCN.
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2.
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(POTENTIAL).
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                                              igh a collaboration -
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There are no restrictions ng as its content is in

http://www.isb-sib.ch/announce/

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NRP1_CHICK
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
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CARBOHYD
                 Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                           16-OCT-2001 (Rel. 40, Neuropilin-1 precursor
                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                       P79795;
01-NOV-1997
                                                                                          NRP1
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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InterPro;
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
          Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                    120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS
                                                                                                                                                                      43
                                                                                                                                                                                       62
                                                                                                                                                                                                        7
                                                                                                                                                                                                                          Ν
                                    OR NRP
                                                                                         CHICK
                                                                                                                                  WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT
                                                                                                                                                                     GYPHSYHPSEKCEWLIQAPEPYQRIIINFNPHFDLEDRD----CKYDYVEVIDGENEGGRL
                                                                                                                                                                                     KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
                                                                                                                                                                                                                       LLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:106206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00754; F5_F8_type_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D50086;
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50060;
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PS01285; FA58C_1;
PS01286; FA58C_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000859; CUB_domain.
IPR000421; FA58_C.
                                                                                                                                                                                                                                                                            923
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA08789:1; --.
                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAM_2;
           Neognathae;
         Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                            103020 MW;
                                                                                                                                                                                                                                                  9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAM_domain
                                                                                                                                                                                                        -----AFRSDKCGG
                                             (A5
                                            sequence update)
annotation update)
protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                        Score 169; DB 1;
Pred. No. 4.5e-06;
1; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                         PROBABLE. PROBABLE.
                                                                                                                                                                                                                                                                                                                               BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    MAM
                                                                                                                                                                                                                                                                                                                                                                                                    F5/8
                                                                                                                                                                                                                                                                                                                                                                                                             CUB
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                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurone; Signal; Repeat; Receptor
                                                                                                                                                                                                                                                                                                                                                 PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUROPILIN-1
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                            TYPE
                                                                                        914
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                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                         Length 923;
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                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                     SIGNAL
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Pred.

No. 6.4e-06;

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DISULFID DISULFID
                                                                                               DISULFID DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developing chick nervous system.";

Dev. Biol. 170:207-222(1995).

-:- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
-:- CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00629; MAM; 1. Pfam; PF00754; F5_F8_type_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY
-i- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-i- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
-i- SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=White leghorn; TISSUE=Embryonic brain; MEDLINE=95324761; PubMed=7601310;
                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00042; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P12259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of a cell adhesion molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G. BLOOD VESSELS IN THE ENTIRE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC
(LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPERTIES
                                                                                                                                                                                                                                                                                                                                    adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000421; FA58_C.
IPR000998; MAM_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000859;
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19
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848
871
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
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801
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171
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9.0%;
28.8%;
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FA58_C.
                                                 MW;
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                                                                                                                 PROBABLE.
PROBABLE.
PROBABLE.
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                Score
                                                                  ВΥ
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                                                                                 PROBABLE.
BY SIMILARITY.
                                                                                                                                                                 MAM
                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                   F5/8
                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                  NEUROPILIN-1
                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                 SIMILARITY.
DD2EE6D6F0CBB68C CRC64;
                                                                                                                                                                                TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsuura T.,
                167;
                                                                                                                                                                                00
                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuboi M., Kawakami
                Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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                PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00122; EGF 1; 1.
PROSITE; PS00122; EGF 1; 1.
PROSITE; PS01186; EGF 2; FALSE_NEG.
Developmental protein; Repeat; Hydrolase;
Metalloprotease; EGF like domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPAN_STRPU
P98068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92315921; PubMed=1618141;
Reynolds S.D., Angerer L.M., Palis J., Nasir A.,
"Early mRNAs, spatially restricted along the anin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAN
    Metalloprotease; SIGNAL 1
                                                                                                                                      PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 2.
SMART; SM00181; EGF; 1.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                                      Pfam; PF01400; Astacin; 1.
                                                                                                                                                                                                                                        Pfam; PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                InterPro; IPR000859;
InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                          EMBL; M84144; AAA30072.1; HSSP; P28825; 1IAF.
                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 114:769-786(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Echino
Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                         MEROPS; M12.013;
                                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 EGF-LIKE DOM
SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: ASYMMETRICALLY ALONG OF THE BLASTULA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             urchin embryos, include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: VERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND HATCHING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSEIILEFESFE-----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OVTE--TISPSVLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVIDGDNAEGRLWGKYCGK-IAPPPLVSSGPYLFIKFVSD-YETHGAGFSIRYEVFKRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKILSPGYLTSPGYPQSYHPSQKCEWLIQAPEPYQRIMINENPHEDLEDRD----CKYDYV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                             IPR000130;
                                                                                                                                                                                                                                                                                                                   IPR001506; Astacin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (Rel. 33, Creat
6 (Rel. 33, Last
8 (Rel. 36, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purpuratus (Purple sea urchin).
; Echinodermata; Eleutherozoa; Echinozoa;
noidea; Echinacea; Echinoida; Strongylocentrotidae;
    16
                                                                                                                                                                                                                                                                              CUB_domain.
EGF-like.
                                                                                                                                                                                                                                                         Zn_MTpeptdse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Palis J., Nasir A., Angerer R.C.; tricted along the animal-vegetal axis one encoding a protein related to tol
    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLY BLASTULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                         Protease;
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                                       Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-CELL
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    RRAAR RAARA
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RESULT 11
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                                                                                            REVISIONS
Kessler E.
                                                                                                                                                                                                                                                                                                                                           PCO1_HUMAN STANDARD; PRT; 449 AA. Q15113; O14550; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Procollagen C-proteinase enhancer protein precursor procollagen COOH-terminal proteinase enhancer) (Type
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               Hirahara I., Syoufuda
Morisaki N., Saito Y.
                                                                                                                                 identification, primary structure, and
cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
                                                                                                                                                                      MEDLINE-95014462; PubMed-7523404;
Takahara K., Kessler E., Binlaminov L., Bruse
Jani-Sait S., Shows T.B., Greenspan D.S.;
"Type I procollagen COOH-terminal proteinase
                                                                                                                                                                                                                              TISSUE=Placenta;
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                         TISSUE=Heart;
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                                                                              Unpublished
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                           Harada K.,
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 procollagen C-protease enhancer
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Pred. No. 7.7e
80; Mismatches
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                           Tomita M., Urakami K.,
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                          Terai H.,
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Pfam; PF01759; NTR; 1
SMART; SM00042; CUB;
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                                                               SEQUENCE
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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1: FUNCTION: BINDS TO THE COCH-TERMINAL PROPERTIDE OF TYPE I PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.

1: FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE METALLOPROTEINASE INHIBITORY ACTIVITY.

1: SUBCELLULAR LOCATION: Secreted.

1: PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Scott I.C., Clark T.G., Takahara K., Hof
"Structural organization and expression
mouse genes for the type I procollagen C
enhancer protein.",
Genomics 55:229-234(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis of 650 kb of genomic reveals 17 genes.";
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Gloeckner G., Gloeckner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000859; CUB_domain.
InterPro; IPR001134; Netrin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteinase enhancer releases a metalloproteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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ion patterns of the human and
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Matches 48; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordi
Mammalia; Eutheria; Rodent
NCBI_TaxID=10116;
                     Pfam; PF00431; CUB; 2.
Pfam; PF00629; MAM; 1.
Pfam; PF00754; F5_F8_type_C; 2
SMART; SM00042; CUB; 2.
SMART; SM000331; FA58C; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00231; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRP2_RAT STANDARD; PRT; 9
035276;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                 EMBL; AF016297; HSSP; P12259; 10
                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                modified and this statement is not removed
                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropilin-2 precursor receptor 2).
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                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                     entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
                                                                                                                                             InterPro;
                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Neuropilin is a semaphorin III receptor."; Cell 90:753-762(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolodkin A.L., Levengood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
              PROSITE; PS50060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282
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                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISO SUBCELLULAR LOCATION: Type I methorane protein.
TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POFTING AND IN OTHER NONNEURONAL TISSUES INCLUDING MILLINING IN THE RIBS.
                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE NEUROPLLIN FAMILY SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTLTTPNWPESDYPPGISCSWHIIAPPDQV-IALTF-EKFDLE--PDTYCRYDSVSVFNG
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                                                                                                                                           IPR000421; FA58_C.
IPR000998; MAM_domain.
                                                                                                                                                                      IPR000859; CUB_domain.
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Glycoprotein; Neurone;
                                                                                                                                                                                               AAC53338.1; -.
             MAM_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce,
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(Vascular endothelial cell growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rowe E.G.,
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Signal; Repeat; Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                         POPULATIONS OF
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PGF.
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TISSUE
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                    NRP2_HUMAN STANDARD,
060462; O14820; O14821;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2010 (Rel. 40, Last annotation update)
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CARBOHYD
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DOMAIN
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                              Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun "Neuropilin-1 is expressed by endothelial and tumor cells isoform-specific receptor for vascular endothelial growth Cell 92:735-745(1998).
                                                                                                                                                                                                                    affinity
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-97470888; I
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
MEDLINE=20309748; PubMed=10748121;
                 CHARACTERIZATION
                                                                                                                 MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                    Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne "Neuropilin-2, a novel member of the neuropilin family, is a h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
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                                                                                                                                                                                                                                                                                                                                                                                           OR VEGF165R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSD-YARQGAGFSLR 138
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                                                                                                                                                                                   19:547-559(1997).
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                                                                                                                                                                                                                                                                    Pubmed=9331348;
                                                                                                                                                                                                                  for the semaphorins Sema E
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Pred.
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CUB 2.
F5/8 T
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CYTOPLASMIC (POTENTIAL)
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NEUROPILIN-2.
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                                                                                                                                                                                                                                                                                                                                       Catarrhini;
                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
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Y SIMILARITY.

A-LINKED (GLCNAC...

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No. 5.
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                                                                                                                                                                                                                  family, is a high
Sema IV but not
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CRC64;
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                           Homo
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                                                               M.;
as an
factor.";
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RT form of vascular endothelial growth factor (VEGF) and of placenta RT growth factor-2, but only neuropilin-2 functions as a receptor for RT the 145-amino acid form of VEGF m; the 145-amino acid form of VEGF m; J. Biol. Chem. 275:18040-18045(2000).

CC -i- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.

CC -i- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.

CC -i- SUBGELLULAR LOCATION: Type I membrane protein.

CC -i- SUBGELLULAR LOCATION: Type I membrane protein.

CC -i- SUBGELLULAR LOCATION: Type I membrane protein.

CC -i- SUBGELLULAR LOCATION: Type I MEMBRANERIC COMPLEX WITH STATEMARTIYE BRODUCTS: 3 ISOFORMS; A22 (SHOWN HERE), A0 AND A17;

CC -i- SIMILARITY: CONTAINS 2 CUB DOMAINS.

CC -i- SIMILARITY: CONTAINS 2 CUB DOMAINS.

CC -I- SIMILARITY: CONTAINS 2 CUB DOMAINS.

CC -I- SIMILARITY: CONTAINS 2 E5/8 TYPE C DOMAINS.
       Har. Hu. Genew; Hu. Genew; Hu. 602070;
                         CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
CONFLICT
                                                                                                                                      DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
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CARBOHYD
CARBOHYD
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DOMAIN
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DOMAIN
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Pfam; PF00754; F5_F8_tyPe_C;
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
Pfam; PFOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF022859; AAC51788 1; -.
EMBL; AF022860; AAC51789.1; -.
EMBL; AF016098; AAC12922.1; -.
HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01180; CUB; PROSITE; PS01285; FA580 PROSITE; PS01286; FA580
                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:8005; NRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01285; FA58C_1;
PS01286; FA58C_2;
PS50060; MAM_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000421;
IPR000998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000859; CUB_domain.
IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rak Z., Cohen T.,
and neuropilin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
       104830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAM_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
MAM.

POLY SER.
BY SIMILARITY.
BY GILCNAC.
N-LINKED (GLCNAC.
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                    CUB
F5/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurone; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR 22 (POTEN NEUROPILIN-2
                                                                                                                                                                                                                                                                                                                                                                    5/8 TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herzog Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 (POTENTIAL).
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                                          ...) (POTENTIAL)
...) (POTENTIAL)
...) (POTENTIAL)
M A17).
M A0).
    CRC64;
                                                                                                                                 .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
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NRP2_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Neuron 19:547-559(1997)

11- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165-145 (1997)

AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.

12- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH NEUROPILLN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.

13- SUBCELLULAR LOCATION: Type I membrane protein.

14- ALTERNATIVE PRODUCTS: 6 ISOFORMS; A22 (SHOWN HERE), A0, A5, A17, A17-ENAMIVE PRODUCED BY ALTERNATIVE SPLICTING.

15- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING GNS, PNS AND IN SOME NONBEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLESS, INTERESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRP2_MOUSE STANDARD; PRT; 931 AA. 035375; 035375; 035374; 035376; 035377; 035378; 16-OCT-2001 (Rel. 40, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Neuropilin-2 precursor (Vascular endothelial cell growth
               EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne "Neuropilin-2, a novel member of the neuropilin family, is a raffinity receptor for the semaphorins Sema E and Sema IV but r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97470888; PubMed=9331348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMYLVMRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS IS DEVELOPMENTALLY REGULATED.
MGI:1100492; Nrp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGAGFSLRYEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEIEKHD---CKYDFIEIRDGDSESADLLGKHCGN-TAPPTIISSGSMLYIKFTSD-YAR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 15
               AF022856;
AF022855;
AF022855;
AF022857;
AF022858;
AF022861;
P12259; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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                             AAC53379.1;
AAC53377.1;
AAC53378.1;
AAC53380.1;
AAC53381.1;
AAC53382.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodentia;
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32.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed. No. 5.8e-05
Mismatches 6
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high
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PROSITE; PS01180; CUB; 2.

PROSITE; PS01285; FA58C_1; 2

PROSITE; PS01286; FA58C_2; 2

PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE
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DISULFID
DISULFID
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CARBOHYD
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VARSPLIC
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DOMAIN
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00431; CUB; 2
Pfam; PF00629; MAM; 1
Pfam; PF00754; F5_F8_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00042; CUB; 2
SMART; SM00231; FA58C;
SMART; SM00137; MAM; 1
                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
131 QGAGFSLRYEI 141
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                                                               76
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                                                                                                                                                                   34
                                                                                                                                                                                                                      Local
                                                                                                                                                     SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER
                                 SEPGFCIHYSI
                                                                 FEIEKHD---CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSD-YAR 130
                                                                                                FGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 153
                                                                                                                                  SGHEVRSQQDPPCGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH
                                                                                                                                                                                                     1 Similarity
43; Conserv
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                                                                                                                                                                                                                                                                        786
931 1
                                                                                                                                                                                                     Conservative
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865
890
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434
642
838
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83
149
                                                                                                                                                                                                                                                                        AA;
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                                 162
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· 104558
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2.
                                                                                                                                                                                                                   8.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FA58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                         MW.
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OF SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N N
                                                                                                                                                                                                   Score 155.5; DB 1;
Pred. No. 5.8e-05;
8; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                     YULALVLHYHRERYAAKKTDHSITYKTSHYINGAPLAVEPT
LTIKLEQERGSHC (IN ISOFORM B0)
VDIPETHGGEGYEDEIDDEYEGDWSNSSSSTSGAGDPSSGK
EKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCTCSYS
GLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA -> G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAM.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                         GILSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA -> GGTLPPGTEPTVDTVPVQPIPAYWYYVMAAGGAVLVLASVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                          EDFKYDIPETHGGEGYEDEIDDEYEGDWSNSSSSTSGAKGD
SSGKEKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCT
CSYSGLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA
-> GTLPPGTEPTVDTVPVQPIPAYWYYMAAGGAVLVLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUB
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                         KLEQERGSHC (IN ISOFORM B5)
G -> I (IN REF. 1; AAC5338
                                                                                                                                                                                                                                                                                                                           ALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurone; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUROPILIN-2.
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                                                                                                                                                                                                                                                                         76F2443F411D2F63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE
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                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Receptor;
                                                                                                                                                                                                                                                                                        AAC53380/AAC53381).
                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                     7;
                                                                                                                                                                                                   Gaps
                                                                                                                                  75
                                                                                                                                                                                                     4;
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RESULT 15 VEGD_RAT

9;

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DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGRR 3 (Flt4) receptor (By similarity).

-: SUBGUILIULAR LOCATION: Secreted (By similarity).

-: SUBGELLULAR COCATION: Secreted (By similarity).

-: PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGRR-3 and VEGRR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGR-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).
              CARBOHYD
CARBOHYD
                                                                                                                                                                                                          PROPEP
CHAIN
PROPEP
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                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley;
Yamada Y., Hirata Y., Nezu J., Shimane M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth factor) (FIGF).
                                                                                                                                                                                                                                                                             PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Glyco
                                                                                                                                                                                                                                                                                                                       Pfam; PF00341; PDGF; 1.
Pfam; PF03128; CXCXC; 1.
ProDom; PD001629; PD_growth_factor;
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF014827; AAB66557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                 Cleavage on
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000072; PD_growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-JUN-2002 (Rel. 41, Created)
L5-JUN-2002 (Rel. 41, Last sequence update)
L5-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and endothelial cell growth, stimulating their proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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 MW;
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N-LINKED
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INTRACHAIN (BY SIMILARITY).
INTRACHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                         VASCULAR ENDOTHELIAL GROWTH FACTOR D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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Search completed: April 29, 2003, 09:06:15 Job time: 13 secs

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